

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2004, 17:09:12 ; Search time 136 Seconds  
(without alignments)

1616.094 Million cell updates/sec

Title: US-09-940-921B-2

Perfect score: 3616

Sequence: 1 MDKYDVIRKAIQGGAFKAYL.....SVSRQEGTKDPYSPVLILM 683

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PTC\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PTC\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3616	100.0	683	9 US-09-940-921B-2	Sequence 2, Appli
2	3431.5	94.9	654	9 US-09-940-921B-4	Sequence 4, Appli
3	3081.5	85.2	640	14 US-10-243-735-2	Sequence 2, Appli
4	3081.5	85.2	640	16 US-10-730-010-2	Sequence 2, Appli
5	2111.5	58.4	403	12 US-10-114-270-188	Sequence 188, App
6	2106.5	58.3	399	12 US-10-114-270-186	Sequence 186, App
7	1106.5	30.6	774	14 US-10-162-706-5	Sequence 5, Appli
8	1081.5	29.9	1214	9 US-09-783-320-4	Sequence 4, Appli
9	1066	29.5	616	14 US-10-243-735-4	Sequence 4, Appli
10	1065	29.5	616	16 US-10-730-010-4	Sequence 4, Appli
11	926.5	25.6	254	10 US-09-898-837A-35	Sequence 35, Appli
12	818	22.6	506	12 US-10-114-270-180	Sequence 180, App
13	816.5	22.6	345	9 US-09-870-962-6	Sequence 6, Appli
14	812	22.5	425	12 US-10-114-270-184	Sequence 184, App
15	812	22.5	489	12 US-10-114-270-182	Sequence 182, App

16	806	22.3	506	12	US-10-415-011-7	Sequence 7, Appli
17	728.5	20.1	459	9	US-09-771-161A-198	Sequence 198, App
18	683	18.9	850	12	US-10-425-114-56926	Sequence 56926, A
19	683	18.9	850	12	US-10-425-114-56928	Sequence 56928, A
20	668	18.5	841	16	US-10-198-070-52	Sequence 52, Appli
21	668	18.5	841	16	US-10-408-765A-1685	Sequence 1685, App
22	668	18.5	841	16	US-10-620-052A-32	Sequence 32, Appli
23	660	18.3	841	14	US-10-198-070-87	Sequence 87, Appli
24	645	17.8	416	9	US-09-731-231A-6	Sequence 6, Appli
25	645	17.8	416	16	US-10-751-985-6	Sequence 6, Appli
26	643	17.8	256	16	US-10-620-052A-48	Sequence 48, Appli
27	638	17.6	260	9	US-09-731-231A-5	Sequence 5, Appli
28	638	17.6	260	16	US-10-751-985-5	Sequence 5, Appli
29	634.5	17.5	713	14	US-10-162-706-2	Sequence 2, Appli
30	634	17.5	692	9	US-09-932-481-2	Sequence 2, Appli
31	634	17.5	692	14	US-10-434-034-2	Sequence 2, Appli
32	633	17.5	698	15	US-10-074-978A-144	Sequence 144, App
33	632.5	17.5	280	14	US-10-162-706-6	Sequence 6, Appli
34	632.5	17.5	460	12	US-10-362-892-23	Sequence 23, Appli
35	632.5	17.5	460	14	US-10-162-706-4	Sequence 4, Appli
36	632.5	17.5	460	15	US-10-288-798-23	Sequence 23, Appli
37	632	17.5	255	10	US-09-898-837A-36	Sequence 36, Appli
38	632	17.5	692	9	US-09-910-150-5	Sequence 5, Appli
39	632	17.5	692	12	US-10-377-097-5	Sequence 5, Appli
40	627.5	17.4	326	15	US-10-074-978A-16	Sequence 16, Appli
41	623	17.2	696	15	US-10-074-978A-146	Sequence 146, App
42	617.5	17.1	291	14	US-10-162-706-17	Sequence 17, Appli
43	617.5	17.1	291	15	US-10-074-978A-145	Sequence 145, App
44	615.5	17.0	253	15	US-10-074-978A-149	Sequence 149, App
45	602	16.6	645	9	US-09-731-231A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-940-921B-2  
; Sequence 2, Application US/09940921B  
; Patent No. US20020147320A1  
; GENERAL INFORMATION:  
; APPLICANT: Fridgle, Carl Johan  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Nepomnichy, Boris  
; APPLICANT: Hu, Yi  
; TITLE OF INVENTION: No. US20020147320alel Human Kinase Proteins and Polynucleotides E  
; FILE REFERENCE: LEX-0227-05A  
; CURRENT APPLICATION NUMBER: US/09/940.921B  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/229,280  
; PRIOR FILING DATE: 2000-08-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 683  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-940-921B-2

Query Match	100.0%;	Score 3616;	DB 9;	Length 683;
Best Local Similarity	100.0%;	Pred. No. 8.6e-245;		
Matches 683;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDKYDVIRKAIQGGAFKAYLAKGKSDSKHCVIKENFEKMPIOKEASKKEVILEKMKH	60	
Db	1	MDKYDVIRKAIQGGAFKAYLAKGKSDSKHCVIKENFEKMPIOKEASKKEVILEKMKH	60	
QY	61	PNIVAFNFSQENGRFLTWMEYCDGDLMKRINFORGVLFSEDIILGFVQISLGLKHII	120	
Db	61	PNIVAFNFSQENGRFLTWMEYCDGDLMKRINFORGVLFSEDIILGFVQISLGLKHII	120	
QY	121	DRKILHRDIKQNTFLSKNGWAKLGDGFIARVLNNSMELARTCIGTPYPLSPICQNKP	180	
Db	121	DRKILHRDIKQNTFLSKNGWAKLGDGFIARVLNNSMELARTCIGTPYPLSPICQNKP	180	



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QY 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYLSPEICQK 180
DB 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYLSPEICQK 180
QY 181 YNNKTDIWSLGCVLVYELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISQLF 240
DB 181 YNNKTDIWSLGCVLVYELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISQLF 240
QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEEFSHMLICRAGAPASRHAGKVQCK 300
DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEEFSHMLICRAGAPASRHAGKVQCK 300
QY 301 IQKVRFGCKPPRSRSVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYD 360
DB 301 IQKVRFGCKPPRSRSVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYD 360
QY 361 YQAQLDMLRRRAHKSYPHPIQENTGVEDYQETRHGSPSPQWPAEYLQKFEAQYK 420
DB 361 YQAQLDMLRRRAHKSYPHPIQENTGVEDYQETRHGSPSPQWPAEYLQKFEAQYK 420
QY 421 VEKOLGLRPSAEPNPNQELRSNGEPRFQELPFRKNEMKEQEWKOLEEIRQOYHND 480
DB 421 VEKOLGLRPSAEPNPNQELRSNGEPRFQELPFRKNEMKEQEWKOLEEIRQOYHND 480
QY 481 MKEIRKMGREPEENSISKHKTLYLVKSNLPHVDASEGEAPVODIEKDLKQMLQNTKE 540
DB 481 MKEIRKMGREPEENSISKHKTLYLVKSNLPHVDASEGEAPVODIEKDLKQMLQNTKE 540
QY 541 SKNPEQYKAKGKVPFENLDCISDENILQBEAMDI PNETLTFFDGMKFEYECVKEH 600
DB 541 SKNPEQYKAKGKVPFENLDCISDENILQBEAMDI PNETLTFFDGMKFEYECVKEH 600
QY 601 GDYTDKAFKHLHCPAAGFSTQT 622
DB 601 GDYTDKAFKHLHCPAAGFSTQT 622
QY 622 GDYTDKAFKHLHCPAAGFSTQT 622
DB 622 GDYTDKAFKHLHCPAAGFSTQT 622
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## RESULT 4

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US-10-730-010-2
; Sequence 2, Application US/10730010
; Publication No. US20040142366A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; OF INVENTION: THEREOF
; FILE REFERENCE: C000121CIPDIV-II
; CURRENT APPLICATION NUMBER: US/10/730,010
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-730-010-2
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Query Match 85.2%; Score 3081.5; DB 16; Length 640;
Best Local Similarity 94.1%; Pred. No. 2.3e-207;
Matches 585; Conservative 2; Mismatches 4; Indels 31; Gaps 1;
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QY 1 MDXYDVITKAIQGAFGKAYLAGKSDSKHCIVKEINFERKPIQEKASKEVILLFKMH 60
DB 1 MDXYDVITKAIQGAFGKAYLAGKSDSKHCIVKEINFERKPIQEKASKEVILLFKMH 60
QY 61 PNIVAFNSQENGRIFIVNEYCDGDLMKRINRQGVLFSEDIILGWVQISLGHKHH 120
DB 61 PNIVAFNSQENGRIFIVNEYCDGDLMKRINRQGVLFSEDIILGWVQISLGHKHH 120
QY 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYLSPEICQK 180
DB 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTICIGTPYLSPEICQK 180
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QY 181 YNNKTDIWSLGCVLVYELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISQLF 240
DB 181 YNNKTDIWSLGCVLVYELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISQLF 240
QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEEFSHMLICRAGAPASRHAGKVQCK 300
DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVIQEEFSHMLICRAGAPASRHAGKVQCK 300
QY 301 IQKVRFGCKPPRSRSVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYD 360
DB 301 IQKVRFGCKPPRSRSVPIKRNAILHRNEWPPAGAKARSIKMIERPKIAAVCGHYD 360
QY 361 YQAQLDMLRRRAHKSYPHPIQENTGVEDYQETRHGSPSPQWPAEYLQKFEAQYK 420
DB 361 YQAQLDMLRRRAHKSYPHPIQENTGVEDYQETRHGSPSPQWPAEYLQKFEAQYK 420
QY 421 VEKOLGLRPSAEPNPNQELRSNGEPRFQELPFRKNEMKEQEWKOLEEIRQOYHND 480
DB 421 VEKOLGLRPSAEPNPNQELRSNGEPRFQELPFRKNEMKEQEWKOLEEIRQOYHND 480
QY 481 MKEIRKMGREPEENSISKHKTLYLVKSNLPHVDASEGEAPVODIEKDLKQMLQNTKE 540
DB 481 MKEIRKMGREPEENSISKHKTLYLVKSNLPHVDASEGEAPVODIEKDLKQMLQNTKE 540
QY 541 SKNPEQYKAKGKVPFENLDCISDENILQBEAMDI PNETLTFFDGMKFEYECVKEH 600
DB 541 SKNPEQYKAKGKVPFENLDCISDENILQBEAMDI PNETLTFFDGMKFEYECVKEH 600
QY 601 GDYTDKAFKHLHCPAAGFSTQT 622
DB 601 GDYTDKAFKHLHCPAAGFSTQT 622
QY 622 GDYTDKAFKHLHCPAAGFSTQT 622
DB 622 GDYTDKAFKHLHCPAAGFSTQT 622
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## RESULT 5

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US-10-114-270-188
; Sequence 188, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytke, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liette, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
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; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 188
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-186

Query Match      58.4%; Score 2111.5; DB 12; Length 403;
Best Local Similarity 99.0%; Pred. No. 1.2e-139;
Matches 399; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MDKYDVIKAGGAFGKAYLAKGSDSKHCVKIENFEKMPQKEASKEVILLKMKH 60
DB 1 MDKYDVIKAGGAFGKAYLAKGSDSKHCVKIENFEKMPQKEASKEVILLKMKH 60

QY 61 PNIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120
DB 61 PNIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120

QY 61 PNIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120
DB 61 PNIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120

QY 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTCTGTPTYSPEICQKP 180
DB 121 DRKILHRDIAQNIIFLSKNGWAKLGDGFIARVLNNSMELARTCTGTPTYSPEICQKP 180

QY 181 YNNKTDIWSLGCYVLELCTLKHPPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSQLF 240
DB 181 YNNKTDIWSLGCYVLELCTLKHPPFEGNNLQQLVLKICQAHFAPISPGFSRELHLSQLF 240

QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEV-IQEFSSHMLICRAGAPASHAGKVQKC 299
DB 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVSEFESHMLICRAGAPASHAGKVQKC 300

QY 300 KIQKRVFQCKPSPRSISVPIKENAILHNEWRPPAGAKARSIRKMERPKIAAVCGHYD 359
DB 301 KIQKRVFQCKPSPRSISVPIKENAILHNEWRPPAGAKARSIRKMERPKIAAVCGHYD 360

QY 360 YYYAQLDMLRRRAHKPSYHPIQENTGVEDYQCTRHGSPSQ 402
DB 361 YYYAQLDMLRRRAHKPSYHPIQENTGVEDYQCTRHGSPSQ 403

RESULT 6
US-10-114-270-186
; Sequence 186, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Zhaozhong
; APPLICANT: Gusev, Vladimir Y.
```



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QY 241 QVSPDRPNSILKPPFLNLPKYLTPVIOEESHMLICRAGAPASRRHAKVVKCK 300
Db 238 QVSPDRPNSILKPPFLNLPKYLTPVIOEESHMLICRAGAPASRRHAKVVKCK 297
QY 301 IQVRFQGGKPPRSRSVPKRNAILHRNEWRPPAGAKARSIMKIERKIAAVCGHYDY 360
Db 298 IQVRFQGGKPPRSRSVPKRNAILHRNEWRPPAGAKARSIMKIERKIAAVCGHYDY 357
QY 361 YYAQLDMLRRRAKPSYHPITPQENTGVEDYGQTRHGPPSQ 402
Db 358 YYAQLDMLRRRAKPSYHPITPQENTGVEDYGQTRHGPPSQ 399

RESULT 7
US-10-162-706-5
; Sequence 5, Application US/10162706
; Publication No. US20030059918A1
; GENERAL INFORMATION:
; APPLICANT: Smolyar, Alex
; TITLE OF INVENTION: Regulation of Human Serine/Threonine
; TITLE OF INVENTION: Kinase
; FILE REFERENCE: 004974.00731
; CURRENT APPLICATION NUMBER: US/10/162,706
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/296,164
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/323,100
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 60/330,578
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/348,601
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-706-5

Query Match 30.6%; Score 1106.5; DB 14; Length 774;
Best Local Similarity 35.2%; Pred. No. 7.2e-69;
Matches 276; Conservative 121; Mismatches 207; Indels 181; Gaps 23;

QY 1 MDKYDVKAIGQAFKAYLAKGSDSKHCIVKINFEKMPIOEAKSKKEVILEKMKH 60
Db 1 MEKYVRLQKIGEGSFGKAYLVKSTEDGRHYVKEINISRMSSDKERQESREAVLANMKH 60
QY 61 PNIVAFNFSQENGRIFIVMEYCDGDLMKRINRQGVLFSEDOILLGWVFOISLGLKHH 120
Db 61 PNIVQKESPEENGSLYIVMDYCEGDLFRKINAQKALFOEDQILDWVFOICLAKHVV 120
QY 121 DRKILHRDIKAQNIPLSKNGMAKLGDFGIARVNNMELARTCIGTPYLSPEICQNK 180
Db 121 DRKILHRDIKSQNIPLTKDGTV-QLGDFGIARVNSTVELARTCIGTPYLSPEICENK 179
QY 181 YNNKTDIWSLGCVLIELCTLKHPEGNLQOLVLIQOAHFAPISGFSREHLSLSOLF 240
Db 180 YNNKSDIWSLGCVLIELCTLKHAFEGAKNMKNLVKISGSPFVPSHYSLRSLLSOLF 239
QY 241 QVSPDRPNSILKPPFLNLPKYLTPVIOEESHMLICRAG- 285
Db 240 KRNPRDPSVNSILEKGFIAKRIEKLFLSPOLIAEEFCLTKSKFGPQLPGKRPASGQGV 299
QY 286 -----APASRRAGKVQVCKTKQVRFQCKCPRRIS--VPKRNAILHRNEWRP 333
Db 300 SSFVPAQKITPAKTYKGYVPLTKYGDKKLEKKPPPKHQAHQIPVK--MNSGEERK 356
QY 334 PAG--AQKARSIMIER----- 348
Db 357 KMSEBAKRRLEFIEKQKQDOIRFLKAEQMKRQEKORLERINRAREQGNVRLRAGG 416
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QY 349 -----PKIAAVCGHYDVVYLAQLDMLRR-RAH-----KPSVHP--IPOE 383
Db 417 SGEVKASFPFGGAVSPSPCPROQYEHYHAIFQMORLRAEDNEARWKGGIYGRWLPER 476
QY 384 NTG---VEDYQGETRHGSPSPQWPAEYLQKXFEAQYQKLVKE-----KOLGLRPSS 431
Db 477 QKGHLAVERAQ-----VEEFQKREAMQNKARAEAGHVYVLARLQIRLQ--- 522
QY 432 AEPNVCNROELR-----SNGEERFQBLPRKKNEMKEQYWKQLEELRQOYHN 479
Db 523 ---NFNERQQIKAKLRGENKEADTKGQEAT-BETDNR---LKQWESLKAQTNARAVALK 575
QY 480 DMKIRKMGREPBENSISKTYLVKKSNIPLVQCDASE-GEAPVQDIEKDKQMLQNT 538
Db 576 EQLERKRKEAVEREKYWEHLVARVKSDDVPLPLELLETGSP----- 619
QY 539 KESKNPEQYKAKGVKFEINLDRKISDENLILQEEBAMDIPNETLT-----PEDGMK 590
Db 620 ---SKQVKPVISVTSALKEVGLDGLTD---TQEEEMKSNISAISSKREILRLNENLK 673
QY 591 FKEVECVKHEGDDYDKAPEKLHCPAGFSTQTVAAVGNRRROWDGGAPQTLQMMAVADIT 650
Db 674 AQEDEKEKQH--HSGSCETVGHKDEREYETEN-AISSDRKKWEMGG-QLVPLDQAVTLDT 729
QY 651 STCPT 655
Db 730 SPSAT 734

RESULT 8
US-09-783-320-4
; Sequence 4, Application US/09783320
; Patent No. US20020038011A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Turner, C. Alexander Jr
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: NO. US20020038011A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0137-USA
; CURRENT APPLICATION NUMBER: US/09/783,320
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,582
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/184,014
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-783-320-4

Query Match 29.9%; Score 1081.5; DB 9; Length 1214;
Best Local Similarity 34.4%; Pred. No. 7.2e-67;
Matches 274; Conservative 129; Mismatches 226; Indels 167; Gaps 21;

QY 1 MDKYDVKAIGQAFKAYLAKGSDSKHCIVKINFEKMPIOEAKSKKEVILEKMKH 60
Db 1 MEKYVRLQKIGEGSFGKAYLVKSTEDGRHYVKEINISRMSSDKERQESREAVLANMKH 60
QY 61 PNIVAFNFSQENGRIFIVMEYCDGDLMKRINRQGVLFSEDOILLGWVFOISLGLKHH 120
Db 61 PNIVQKESPEENGSLYIVMDYCEGDLFRKINAQKALFOEDQILDWVFOICLAKHVV 120
QY 121 DRKILHRDIKAQNIPLSKNGMAKLGDFGIARVNNMELARTCIGTPYLSPEICQNK 180
Db 121 DRKILHRDIKSQNIPLTKDGTV-QLGDFGIARVNSTVELARTCIGTPYLSPEICENK 179
QY 181 YNNKTDIWSLGCVLIELCTLKHPEGNLQOLVLIQOAHFAPISGFSREHLSLSOLF 240
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Db 121 DRKILHRTKSONIFUTKQGTV-QLGDFGIARVLNSTVELARTCTGTPTTYSPEICENKP 179  
QY 181 YNNKTDINSLGCVLYELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLF 240  
Db 180 YNNKSDIWAIGCVLYELCTLKHAFAGNNKNVLKLIISGSPFPVSPHYSYDLRSLSOLF 239  
QY 241 QVSPDRPSINSILKPPFLNIPKLTPEVICQEFSHMLICRAG----- 285  
Db 240 KRNFRDRPSVNSILEKGFIAKIEKFLSPQLAEBFCLTKLSKFGPQLPGKRPSGGQV 299  
QY 286 -----APASRHAGVWQCKIQKVFQCKPPRSRIS--VPIKRNAILHNEWRP 333  
Db 300 SSVFPAQKTKPAAKYGVLTYYKYGDKLLEKPPKHKQAHQIPVK--MNSGEERK 356  
QY 334 PAG-AQKARSIMIER----- 348  
Db 357 KMSEEAARKRLLEFIEFEKQKQDQIRFLKAEQMKRQEKQRLRINRAEQGWRNVLRAGG 416  
QY 349 -----PKIAAVCGHYDYAQLDMLRR-RAH-----KPSVHP-IPQE 383  
Db 417 SGEVKASFFGIGGAVSPSCSPGQYEHYHALFDQMORLAEDNEARWKGGIYGRWLPER 476  
QY 384 NTG---VEDYQETRHPSPSPQWPAFYLQKFEAQYKLVK-----KOLGLRPSS 431  
Db 477 QXGHLAVERANQ-----VEBFLOKREAMQNKARAGHVYVLARLQIRLQ--- 522  
QY 432 AEPNNYQREL-----SNGEPRQELPPFRKNEMKEQYKQLEBEIQQOYHN 479  
Db 523 ---NFNERQIQAKURGENKEADGTGQBAT-EETDMR---LKKMESLKAQTNARAALVK 575  
QY 480 DMKEIRKMGREPEENSKISHKTYLVKKNLPV 512  
Db 576 EQLERKRKEAYERKKVWEHLVARVKSSDVPL 608

## RESULT 11

US-09-898-837A-35  
; Sequence 35, Application US/09898837A  
; Publication No. US2003007697A1  
; GENERAL INFORMATION:  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Vernet, Corine  
; APPLICANT: Herrmann, John L.  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Taupier, Jr., Raymond  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Curagen Corporation  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: MacDougall, John R.  
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND  
; FILE REFERENCE: 15966-598 CIP  
; CURRENT APPLICATION NUMBER: US/09/898, 837A  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906  
; PRIOR FILING DATE: 2000-07-03

## RESULT 12

US-10-114-270-180  
; Sequence 180, Application US/10114270  
; Publication No. US20040030110A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Liu, Ziaohong  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Li, Li  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Smithson, Glennnda  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Taupier, Jr., Raymond J.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Anderson, David W.  
; APPLICANT: Liete, Mario W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Stone, David J.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Rothenberg, Mark E.  
; TITLE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-322C  
; CURRENT APPLICATION NUMBER: US/10/114,270

; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-898-837A-35  
Query Match 25.6%; Score 926.5; DB 10; Length 254;  
Best Local Similarity 66.8%; Pred. No. 7.2e-57;  
Matches 169; Conservative 41; Mismatches 42; Indels 1; Gaps 1;  
QY 7 IKALQGAFGKAYLAKSKSDSKVCIKKEINFEKMPIOEASKEVILLKMKHPNIVAF 66  
Db 3 LQKTGEGSFGKAVJAVKSTEDGRHYVKEINISMSDKERQESRREVAVLANMKHPNIVQY 62  
QY 67 FNSFOENGRIFIVMEYCDGGDLMKRINRQRGVLFSEQILGWFWQISLGLKHIHDRKILH 126  
Db 63 KESFEENGSLYIVNDYCEGGDLFKRINAQKALFQEQILDMFWQICLALKVHVDKILH 122  
QY 127 RDIKAQNFISKGNWAKLGDGFGIARVLNNSMELARTCTGTPTTYSPEICENKPNKTD 186  
Db 123 RDIKSONIFLTQKQTV-QLGDFGIARVLNSTVELARTCTGTPTTYSPEICENKPNKSD 181  
QY 187 IWSLGCVLVYELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISOLFQVSPDR 246  
Db 182 IWAIGCVLYELCTLKHAFAGNNKNVLKLIISGSPFPVSPHYSYDLRSLSOLFQVSPDR 241  
QY 247 RPSINSILKRPFL 259  
Db 242 RPSVNSILEKGF1 254

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; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 180
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-180

Query Match          22.6%; Score 818; DB 12; Length 506;
Best Local Similarity 34.4%; Pred. No. 6.9e-49;
Matches 198; Conservative 97; Mismatches 178; Indels 102; Gaps 16;

QY 1 MDKYDVKAIGQAFKAYLAKGSDSKHCIVKEINFEKMPIOEKEASKEVILLKMKH 60
Db 1 MDDYVLMRIGEGSFGALLVQHSSNQWFMKEIRLPKVTNTQN-SRKEAVLLAKMKH 59

QY 61 PNIVAFNSFOENGRLFIVMEYCDGDLMKRINRQGVLPFSDQILGWVQISGLKHH 120
Db 60 PNIVAFKFEAEGLHYIVMEYCDGDLMKQIKQKQKGLFPEDQILNFTQCLGVNHH 119

QY 121 DRKILHRDIKAQNIPLSKNGWAKLDFGFIARVLNNSMELARTCTGTPTVYLSPEICNKP 180
Db 120 KKEVLHRDIKSQNIPLTQNGKV-KLGDGFSARLLSNPMAFACTYGTPTVYLPPELWNL 178

QY 181 YNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLTICQAHFAPISPGFSRHLISQLP 240
Db 179 YNKSIDWSLGCILVELCTLKHPFGANSWKNILKVCQCISPLSPSHYSYELQFLVKQMF 238

QY 241 QVSPDRPSINSILKPPLENLIPKYLTPETVIOEFSHMLICRAGAPASRHAGKVQCK 300
Db 239 KRNFSHRPATLLSGRIVARLVQKCLPEIINE-VOEVEIEIK 282

QY 301 IQKVRPQKCPPRSRIKRNAILHRNEWRPPAGAOKARSIKMIEPKIAVCGHYDY 360
Db 283 NGSKHTPRKTNPSRIRIALGNEASTVQEEQDRKGS----- 319

QY 361 YYAQDLMLRRRAHKSYPHPPOENTGVEDYGOETRHGSPS-----QWPAEYLQRKFEAQ 416
Db 320 -HTDUESINENIUVESALRRVNEEGK--NKSVHLRKASSPNLHRKQW----- 363

QY 417 YKLKVEKQIQLRPPSAEPNINQBELRSN--GEEPR-FQELPPFRKNEKQYKQLEEI 473
Db 364 -----EKNV-----PNTALTALENASILTSSLTAEDDRGGSVIKYKNTTRKQ--W-LKET 411

QY 474 RQYVNDKMEIKKVGREPEENSKISHKTYLV-----KKSNIPLVHQDASEG-----E 520
Db 412 PTLNLNLK-----NADLSAFQTYTYRFGSEGLKPLSETEASDSVDGHD 461

QY 521 APVQD---IEKDLKQWLQNTKESNPQKVKAKK 552
Db 462 SVILQPERLEPLGDEEDTDTEEDDNDPWSLKK 496
```

```

RESULT 13
US-09-870-962-6
; Sequence 6, Application US/09870962
; Patent No. US20020081290A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Valda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/870,962
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 09/420,915
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/173,581
; PRIOR FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1567782
US-09-870-962-6

Query Match          22.6%; Score 816.5; DB 9; Length 345;
Best Local Similarity 44.9%; Pred. No. 5.4e-49;
Matches 173; Conservative 55; Mismatches 80; Indels 77; Gaps 6;

QY 1 MDKYDVKAIGQAFKAYLAKGSDSKHCIVKEINFEKMPIOEKEASKEVILLKMKH 60
Db 1 MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVKEINISRMSSKERESREYAVLANMKH 60

QY 61 PNIVAFNSFOENGRLFIVMEYCDGDLMKRINRQGVLPFSDQILGWVQISGLKHH 120
Db 61 PNIVQVRESF-----EGILDWVQICLALKVH 88

QY 121 DRKILHRDIKAQNIPLSKNGWAKLDFGFIARVLNNSMELARTCTGTPTVYLSPEICNKP 180
Db 89 DRKILHRDIKSQNIPLTQNGTV-QLGDGFIARVLNSTVELARTCTGTPTVYLSPEICENKP 147

QY 181 YNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLTICQAHFAPISPGFSRHLISQLP 240
Db 148 YNKSIDWALGCVLYELCTLKHPFAGSWKNLVLIISGSPFVSHYSDRLSVQLP 207

QY 241 QVSPDRPSINSILKPPLENLIPKYLTPETVIOEFSHMLICRAGAPASRHAGKVQCK 293
Db 208 KRNPRDRPSVNSILEKGFIAKRIEKLSPQIAEBEFLCTFKSGSQIPAKRPASGQNS 267

QY 294 -----KVQCKIKQVRFQKCPPRSRIKRNAIL 325
Db 268 ISVMPAQKTKPAKYGIPLAYKYGDKLKKHKKPLQGHK-QAHQTPKRVNTGERRKI 326

QY 326 LHRNEWRPPAGAOKARSIKMIEPRK 350
Db 327 SEB-----AARKRLEFIEKDK 343
```

```

RESULT 14
US-10-114-270-184
; Sequence 184, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
```



```

; SEQ ID NO 182
; LENGTH: 489
; TYPE: FRT
; ORGANISM: Homo sapiens
US-10-114-270-182

Query Match      22.5%; Score 812; DB 12; Length 489;
Best Local Similarity 54.7%; Pred. No. 1.7e-48;
Matches 150; Conservative 52; Mismatches 70; Indels 2; Gaps 2;

Qy 1 MDKYDVKAIGQAGKAYLAKGSDSKHCVIKEINFERMPIQEKEASKKEVILLKMKH 60
Db 1 MDDYVLRMIGEGSFGALLVQHESNQMFAMKEIRLPKVTNTQN-SRKEAVLLAKMKH 59

Qy 61 PNIVAFENSGFOENGRIFVMEYCDGDLMKRINRQGVLFSEDOILGNFVOISIGLKH 120
Db 60 PNIVAFKESFEAGHDIYVNEYCDGDLQKIKQKQKGLFPEDQILNWFQCLGVNHH 119

Qy 121 DRKILHRDIKAQNIFLSKNGMYAKLGDGFIARVLNNSMELARTCIGTPTPYLSPEICONKP 180
Db 120 KKEVLHRDIKSNIFLTQNGV-KLGDGFGSARLLSNPMAFACTYVGTPTPYVPEIWEINLP 178

Qy 181 YNKTDIWSLGCVLVELCTLKHPPFEGNLLQQLVLKICQAHFAPISFGFSRELHSLISOLF 240
Db 179 YNKSIDIWSLGCILYELCTLKHPPFQANSWKNILKVCQGCISPLFSHYSEYELQFLVKQMF 238

Qy 241 QVSPRDRPSINSILKRPFLLENLIPKYLTPETVIOE 274
Db 239 KNPFSRPSATLLSRGIVARLVQKCLPPEIIME 272

```

Search completed: October 8, 2004, 17:20:45  
Job time: 139 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2004, 17:00:40 / Search time 62 Seconds  
(without alignments)  
3112.590 Million cell updates/sec

Title: US-09-940-921B-2  
Perfect score: 3616  
Sequence: 1 MDKYDVKAIGQAFKAYL.....SVSRQEGTKDPYSPVLIM 683

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3616	100.0	683	5	Aau77928 Amino aci
2	3431.5	94.9	654	5	Aau77929 Amino aci
3	3081.5	85.2	640	6	Abg72000 Human ser
4	2925	80.9	649	4	Aau03545 Human pro
5	2820	78.0	631	6	Abp71710 Human NEK
6	2111.5	58.4	403	6	Abu54635 Human NOV
7	2106.5	58.3	399	6	Abu54634 Human NOV
8	1118.5	30.9	544	6	Abp96073 Human pro
9	1106.5	30.6	774	6	Aao26613 Serine/th
10	1106.5	30.6	774	6	Abp71711 NEK-like
11	1106.5	30.6	774	6	Aao16441 Human ser
12	1106.5	30.6	774	6	Abp97691 Amino aci
13	1105.5	30.6	1242	4	Ram33210 Human pol
14	1105.5	30.6	1242	6	Aao16440 Human ser
15	1081.5	29.9	1214	4	Aao07102 Human nov
16	1077.5	29.8	1214	4	Ram33211 Human pol
17	1077.5	29.8	1214	6	Abu08113 Human kin
18	930.5	25.7	632	5	Abp55160 Ser/Thr/T
19	818	22.6	506	6	Abu54631 Human NOV
20	816.5	22.6	345	3	Aay76753 Human pro
21	816.5	22.6	345	4	Aao08211 Human pro
22	816.5	22.6	345	5	Abb84438 Human pro
23	812.5	22.5	546	6	Abp96072 Human pro
24	812	22.5	425	6	Abu54633 Human NOV
25	812	22.5	489	6	Abu54632 Human NOV

26	808.5	22.4	511	6	Abp71712 NEK-like
27	808.5	22.4	511	6	Abp97690 Amino aci
28	808	22.3	506	4	Aam78344 Human pro
29	808	22.3	506	5	Abp60668 Human ser
30	806	22.3	506	5	Aae24136 Human kin
31	804.5	22.2	507	6	Abp97688 Amino aci
32	804	22.2	527	4	Aam79328 Human pro
33	804	22.2	527	5	Abb97224 Novel hum
34	800	22.1	489	7	Adc99067 Human KPP
35	741.5	20.5	510	3	Aay68778 Amino aci
36	728.5	20.1	459	6	Abp71713 NEK-like
37	728.5	20.1	459	6	Abp97689 Amino aci
38	668	18.5	841	7	Adb37570 Neural th
39	660	18.3	841	7	Adb37570 Neural th
40	636.5	17.6	329	6	Aao26614 Human ser
41	634.5	17.5	713	6	Aao26615 Human ser
42	634	17.5	692	5	Aao19418 Human ser
43	632.5	17.5	280	6	Aao26612 Human ser
44	632.5	17.5	460	5	Aae21728 Human PKI
45	632.5	17.5	460	6	Aao26616 Human ser

ALIGNMENTS

RESULT 1  
AAU77928  
ID AAU77928 standard; protein; 683 AA.  
XX  
AC AAU77928;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Amino acid sequence for novel human kinase protein #1.  
XX  
KW Novel human protein; NHP; serine-threonine kinase; brain;  
KW calcium/calmodulin-dependent kinase; myosin light chain kinase;  
KW biological disorder; spleen; placenta; chromosome 6; enzyme.  
XX  
OS Homo sapiens.  
XX  
FN WO200218555-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 28-AUG-2001; 2001WO-US026776.  
XX  
PR 31-AUG-2000; 2000US-0229280P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
PI Fridge CJ, Hilbun E, Nepomnichy B, Hu Y;  
XX  
DR WPI; 2002-292200/33.  
XX  
N-PSDB; ABK12424.  
XX  
Novel polynucleotide encoding novel human protein sharing structural similarity with animal kinases e.g. serine-threonine, calcium/calmodulin-dependent, and myosin light chain kinases, useful as probes and primers.  
XX  
Claim 1; Page 38-39; 46pp; English.  
XX  
The present invention relates to the isolation of novel human proteins (NHPs) and the polynucleotide sequences encoding them. The NHPs of the invention are kinase proteins and share structural similarity to serine-threonine, calcium/calmodulin-dependent, and myosin light chain kinases. The sequences of the invention are useful for treating biological disorders. The polynucleotide sequences encoding the kinase proteins can be used as primers and probes. The sequences are also useful for identifying mutations associated with a particular disease and also in a prognostic or diagnostic assay. The present sequence represents human protein kinase #1 which is expressed in a broad range of human tissues such as brain, spleen, and placenta. The gene encoding protein kinase #1

[illegible]



Db 465 -----ENSKISHKTYLVKSNLPHVQDASEGAFVQIEKDLQVRLQNTKE 511  
QY 541 SKNPEQKYKAKGVKFEINLDCISDENILQEEAWDIPNETILTPEDEGMKFKYECVKEH 600  
Db 512 SKNPEQKYKAKGVKFEINLDCISDENILQEEAWDIPNETILTPEDEGMKFKYECVKEH 571  
QY 601 GYTDKAFKLHCPEAGFSTQTVAAVGNRRQDGGAPQTLLOWMAVADITSTCTGPDSE 660  
Db 572 GYTDKAFKLHCPEAGFSTQTVAAVGNRRQDGGAPQTLLOWMAVADITSTCTGPDSE 631  
QY 661 SVLSVSRQEGKTKDPYSPVLILM 693  
Db 632 SVLSVSRQEGKTKDPYSPVLILM 654  
RESULT 3  
ABG72000  
ID ABG72000 standard; protein; 640 AA.  
XX  
AC ABG72000;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Human serine/threonine kinase.  
XX  
KW Human; enzyme; serine/threonine kinase; lung carcinoma; chromosome 13.  
XX  
OS Homo sapiens.  
XX  
FN WO200281727-A2.  
XX  
XX 17-OCT-2002.  
XX  
XX 02-APR-2002; 2002WO-US010156.  
XX  
XX 03-APR-2001; 2001US-00824583.  
XX  
XX 05-JUN-2001; 2001US-00873404.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Webster M, Yan C, Di Francesco V, Beasley EM;  
XX  
XX WPI; 2003-058562/05.  
XX  
XX N-PSDB; ABS57149, ABS57150.  
XX  
XX Novel human kinase protein expressed in lung carcinoma and placenta is  
XX  
XX useful to diagnose and treat diseases and disorders associated with  
XX  
XX expression or activity of the protein.  
XX  
XX Claim 1; Fig 2A; 101pp; English.  
XX  
XX The invention relates to an isolated human kinase peptide of the  
XX  
XX serine/threonine, an allelic variant or orthologue, and encoded by a  
XX  
XX nucleic acid that hybridises under stringent conditions with the cDNA and  
XX  
XX gene sequences appearing as ABS57149 and ABS57150, or a fragment  
XX  
XX comprising at least 10 contiguous amino acids. Also included are an  
XX  
XX antibody that selectively binds to the kinase, a gene chip comprising the  
XX  
XX nucleic acids, a transgenic non human animal comprising the nucleic  
XX  
XX acids, a nucleic acid vector comprising the nucleic acids, a host cell  
XX  
XX containing the vector and expressing the kinase, identifying a  
XX  
XX modulator/binding agent of the kinase (comprising contacting the peptide  
XX  
XX with an agent and determining if the agent has modulated function,  
XX  
XX expression or activity of the peptide or formed a complex with it), The  
XX  
XX molecules of the invention are useful to diagnose and treat a disorder  
XX  
XX characterised by aberrant expression of the protein (e.g. lung  
XX  
XX carcinoma). Agents which modulate the function or activity of the protein  
XX  
XX are useful to treat diseases or disorders mediated by human kinase  
XX  
XX protein. The gene for encoding the novel kinase is located on chromosome  
XX  
XX 13. The present sequence represents the novel human kinase  
XX  
XX Sequence 640 AA;

Query Match 85.2%; Score 3081.5; DB 6; Length 640;  
Best Local Similarity 94.1%; Pred. No. 8.1e-233;  
Matches 585; Conservative 2; Mismatches 4; Indels 31; Gaps 1;  
QY 1 MDKVDVTKAQGGAFKAYLAKGSKDSKHCYVKEINPEKMPIOEKEASKKEVILLEKWKH 60  
Db 1 MDKVDVTKAQGGAFKAYLAKGSKDSKHCYVKEINPEKMPIOEKEASKKEVILLEKWKH 60  
QY 61 PNIVAFNSFOENGRLFIWMEYCDGGDLMKRINRQGVLFSEDOILGFWFQISLGLKHIH 120  
Db 61 PNIVAFNSFOENGRLFIWMEYCDGGDLMKRINRQGVLFSEDOILGFWFQISLGLKHIH 120  
QY 121 DRKILHRDIKAQNTFLSKNGWAKLGFAGIARVLNNSMELARTICIGTPYLSPEICQK 180  
Db 121 DRKILHRDIKAQNTFLSKNGWAKLGFAGIARVLNNSMELARTICIGTPYLSPEICQK 180  
QY 181 YNNKTDIWSLGCVLVELCTLKHPPPEGNLQOLVLIQCAHFAPISPGFSRSLHSLSOLF 240  
Db 181 YNNKTDIWSLGCVLVELCTLKHPPPEGNLQOLVLIQCAHFAPISPGFSRSLHSLSOLF 240  
QY 241 QVSPDRPSINSILKRPFLNLIPIKYLTPEVIOEFSHMLICRAGAPASHAGKVKQCK 300  
Db 241 QVSPDRPSINSILKRPFLNLIPIKYLTPEVIOEFSHMLICRAGAPASHAGKVKQCK 300  
QY 301 IQKVRFGKCPPRSIRISVPINRNLHNRNWRPPAGAKARSIKMIERPKIAAVCGHYDY 360  
Db 301 IQKVRFGKCPPRSIRISVPINRNLHNRNWRPPAGAKARSIKMIERPKIAAVCGHYDY 360  
QY 361 YYAQLDMLRRRAHKPSYHPIQENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 420  
Db 361 YYAQLDMLRRRAHKPSYHPIQENTGVEDYQGETRHGSPSPQWPAEYLQKFEAQYK 420  
QY 421 VEKOLGLPSSAEPNPNQRLNSGEBEPPELPPFRKNENKKEQYWKQLEIEIQOYHND 480  
Db 421 VEKOLGLPSSAEPNPNQRLNSGEBEPPELPPFRKNENKKEQYWKQLEIEIQOYHND 480  
QY 481 MKEIRKMGREPE-----DIEKDLQKMLQNTKE 540  
Db 481 MKEIRKMGREPE-----DIEKDLQKMLQNTKE 509  
QY 541 SKNPEQKYKAKGVKFEINLDCISDENILQEEAWDIPNETILTPEDEGMKFKYECVKEH 600  
Db 510 SKNPEQKYKAKGVKFEINLDCISDENILQEEAWDIPNETILTPEDEGMKFKYECVKEH 569  
QY 601 GYTDKAFKLHCPEAGFSTOT 622  
Db 570 GYTDKAFKLHCPEAGFSTOT 591  
RESULT 4  
AAU03545  
ID AAU03545 standard; protein; 649 AA.  
XX  
AC AAU03545;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human protein kinase #45.  
XX  
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
KW metabolic disorder; immune related disease; neurological disorder;  
KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
KW reproductive disorder.  
XX  
OS Homo sapiens.  
XX  
FN WO200139503-A2.  
XX  
XX 31-MAY-2001.  
XX  
XX 22-NOV-2000; 2000WO-US032085.  
XX  
XX 24-NOV-1999; 99US-0167482P.  
XX  
PR

XX PA (SUGEN-) SUGEN INC.

XX PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

XX PI Flanagan P, Clary D;

XX DR WPI; 2001-343950/36.

XX DR N-PSDB; AAS06745.

XX PT Nucleic acids encoding human kinase polypeptides, useful for preventing

XX PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and

XX PT neuronal-associated diseases, and microbial infections.

XX PS Claim 7; Fig 2; 433pp; English.

XX CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel

XX CC protein kinases have been identified as members of the tyrosine or

XX CC serine/threonine kinase (STK and STK) families. The polynucleotides

XX CC encoding protein kinases and the polypeptides may be used in the

XX CC prevention, diagnosis and treatment of diseases associated with

XX CC inappropriate kinase expression. For example, they may be used to treat

XX CC cancers (especially cancers of haematopoietic origin), cardiovascular

XX CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

XX CC immune related diseases (e.g. rheumatoid arthritis), neurological

XX CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.

XX CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious

XX CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

XX CC Additionally, polynucleotides encoding protein kinases may be used for

XX CC gene therapy and as DNA probes in diagnostic assays. The protein kinase

XX CC polypeptides may be used as antigens in the production of antibodies

XX CC against the protein kinases and in assays to identify modulators of

XX CC protein kinase expression and activity

XX SQ Sequence 649 AA;

Query Match 80.9%; Score 2925; DB 4; Length 649;

Best Local Similarity 84.2%; Pred. No. 1.6e-220;

Matches 570; Conservative 12; Mismatches 31; Indels 64; Gaps 6;

QY 1 MDKYDVKAIGQAGAFKAYLAKGKSDSKHCVCKEINFERMPIQEKAEKKEVILLEKMKH 60

DB 1 MDKYDVKAIGQAGAFKAYLAKGKSDSKHCVCKEINFERMPIQEKAEKKEVILLEKMKH 60

QY 61 PNIVAFNSFOENGRFLFYMEYCDGDLMKRINRQGVLFSDQILGFWFVLSLGLKHIH 120

DB 61 PNIVAFNSFOENGRFLFYMEYCDGDLMKRINRQGVLFSDQILGFWFVLSLGLKHIH 120

QY 121 DRKILHRDIAQNIIFLSKNGWAKLGFQIARVLNNSMELARTCTGTYPYLSPEICQNKP 180

DB 121 DRKILHRDIAQNIIFLSKNGWAKLGFQIARVLNNSMELARTCTGTYPYLSPEICQNKP 180

QY 181 YNKTDIWSLGCVLVELCTLKHPPFENNLIQVLVKICQAHFAPISPGFSRSLHLSISQLF 240

DB 181 YNKTDIWSLGCVLVELCTLKHPPFENNLIQVLVKICQAHFAPISPGFSRSLHLSISQLF 240

QY 241 QVSPDRPINSILKRPFLNLIPLYLTPETIQEE- - -FSHMLICRAGAPASRAGKV 296

DB 241 QVSPDRPINSILKRPFLNLIPLYLTPETIQEE- - -FSHMLICRAGAPASRAGKV 296

QY 297 QKCKIQKVFQKCPSPRSISVPIKRNAILHRNEWRPAGAKAFSIXMIERPKIAAVCG 356

DB 297 QKCKIQKVFQKCPSPRSISVPIKRNAILHRNEWRPAGAKAFSIXMIERPKIAAVCG 356

QY 357 HYDYTYAQLDMLRRRAHKPSYHPIQENTGVEDYQETHGSPSPQWPAEYLQKFEFAQ 416

DB 357 HYDYTYAQLDMLRRRAHKPSYHPIQENTGVEDYQETHGSPSPQWPAEYLQKFEFAQ 416

QY 417 YKLKVEKQLGLRPPSAEPNQNORLRSNGEPPFQELPPFRKNEMKEQYWKQLEERQ 476

DB 417 YKLKVEKQLGLRPPSAEPNQNORLRSNGEPPFQELPPFRKNEMKEQYWKQLEERQ 476

QY 477 YHNDMKEIRKKGREPE- - - - -DIEKDLKQWRLQ 480

DB 477 YHNDMKEIRKKGREPE- - - - -DIEKDLKQWRLQ 480

DB 452 YHNDMKEIRKKGREPE- - - - -DIEKDLKQWRLQ 480

QY 537 NTKSKNPEQYKAKGKVKFEINLDKICISDENILQEEAMDIPNETLTFFDGMKFEYEC 596

DB 481 NTKSKNPEQYKAKGKVKFEINLDKICISDENILQEEAMDIPNETLTFFDGMKFEYEC 540

QY 597 VKHGDYTDKAFKELHCFEAGFSTQTTVAANGNRQWDGGAPQTLQWMAVADITSCTPTG 656

DB 541 VKHGDYTDKAFKELHCFEAGFSTQTTVAANGNRQWDGGAPQTLQWMAVADITSCTPTG 600

QY 657 PDSSEVLSVSRQEGKTK 673

DB 601 PDNGQVIVIEGIPGNRK 617

RESULT 5

ABP71710

ID ABP71710 standard; protein; 631 AA.

XX AC ABP71710;

XX DT 17-APR-2003 (first entry)

XX DE Human NEK-like serine/threonine protein kinase # SEQ ID 2.

XX KW Human; NEK-like serine/threonine protein kinase; cytostatic; cardiant;

XX KW antiinflammatory; nootropic; neuroprotective; cancer; colon cancer;

XX KW cardiovascular disorder; diabetes; COPD; CNS disorder.

XX OS Homo sapiens.

XX FN WO2003000903-A2.

XX PD 03-JAN-2003.

XX PF 24-JUN-2002; 2002WO-EP006948.

XX PR 25-JUN-2001; 2001US-0300068P.

XX PR 07-DEC-2001; 2001US-0336704P.

XX PA (FARB ) BAYER AG.

XX PI Xiao Y;

XX DR WPI; 2003-184051/19.

XX DR N-PSDB; ABZ59716.

XX PT New polynucleotide encoding a NEK-like serine/threonine kinase

XX PT polypeptide useful for treating diseases associated with kinase

XX PT dysfunction, e.g. cardiovascular disorders, cancer such as colon cancer,

XX PS diabetes and CNS disorders.

XX PS Claim 1 a ii; Fig 2; 149pp; English.

XX CC The invention relates to a newly isolated polynucleotide encoding an NEK-

XX CC like serine/threonine protein kinase. The activity of the polynucleotide

XX CC and polypeptide of the invention may be described as cytostatic,

XX CC cardiant, antiinflammatory, nootropic and neuroprotective. The expression

XX CC vector and reagent of the invention are useful for the preparation of a

XX CC medicament for modulating the activity of an NEK-like serine/threonine

XX CC kinase in a disease, such as cancer (e.g. colon cancer), cardiovascular

XX CC disorder, diabetes, COPD or CNS disorder. The polypeptides may also be

XX CC used to identify compounds which may act as activators or inhibitors at

XX CC the enzyme's active site, to raise specific antibodies which can block

XX CC the enzyme and effectively reduce its activity, as a bait protein in a

XX CC two-hybrid or three-hybrid assay to identify other proteins which bind to

XX CC or interact with the human NEK-like serine/threonine kinase polypeptide

XX CC and modulate its activity, and for the immunisation of mammals. The

XX CC current sequence represents the human NEK-like serine/threonine protein

XX CC kinase of the invention

XX SQ Sequence 631 AA;

Query Match		78.0%; Score 2820; DB 6; Length 631;
Best Local Similarity		79.8%; Pred. No. 2.6e-212;
Matches 552; Conservative		9; Mismatches 19; Indels 112; Gaps 5;
QY	1	MDKYDVIRKAIGQAGFKAYLAKGSDSKHCVIKIEINFEKMPIQEKEASKEVILLERKMH 60
Db	1	MDKYDVIRKAIGQAGFKAYLAKGSDSKHCVIKIEINFEKMPIQEKEASKEVILLERKMH 60
QY	61	PNIVAFNSFOENGRLFIWMECDGDLKRNORGVLFSEDDILGHFWQISLGLKHIIH 120
Db	61	PNIVAFNSFOENGRLFIWMECDGDLKRNORGVLFSEDDILGHFWQISLGLKHIIH 120
QY	121	DRKILHRDIKAQNIIFLSKNGMAKLGDFGIARVLNNSMELARTCIGTPIYLSPEICQNK 180
Db	121	DRKILHRDIKAQNIIFLSKNGMAKLGDFGIARVLNNSMELARTCIGTPIYLSPEICQNK 180
QY	181	YNNKTDIWSLGVLYELCTLKHPFEGNNLQVLKICQAHFAPISPGFSRSLHSLSOLF 240
Db	181	YNNKTDIWSLGVLYELCTLKHPFEGNNLQVLKICQAHFAPISPGFSRSLHSLSOLF 240
QY	241	QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEBSFHWMLICRAGAPASRHAGKVQVK - 298
Db	241	QVSPDRPSINSILKRPFLNLI PKYLTPEVIOEBSFHWMLICRAGAPASRHAGKVQVQHT 300
QY	299	-----CKIQKRVFGKCPPRSRISVPIKRNAILHRNEWPPAGAQAQKAR 341
Db	301	GVRSGLSRPWAALLRLCRLQLRL-----LSQAAVECLR-----LF 337
QY	342	STKMLERPKIAVCGHYDYVYLAOLMRRRAHKPSYHPIPOENTGVEDYGOETRHGPS 401
Db	338	QIKMLERPKIAVCGHYDYVYLAOLMRRRAHKPSYHPIPOENTGVEDYGOETRHGPS 397
QY	402	QWPAEYLQKFAAQYKLVKVEKQLGRFSSAEPNTNQRQLRSNGEERFOELPFRKNEM 461
Db	398	QWPAEYLQKFAAQYKLVKVEKQL-----421
QY	462	KEQEVYKQLEBEIROQYHNDKMEIRKNGREPEENSKIHKTYLVKSNLPVHQDASEGEA 521
Db	422	---EYWKQLEBEIROQYHNDKMEIRKNGREPE-----450
QY	522	PVQDIEKDLQMLQNTKESKNPEQYKAKGVKFEINLDCISDENILOEEAAMDIPNE 581
Db	451	---DIEKDLQMLQNTKESKNPEQYKAKGVKFEINLDCISDENILOEEAAMDIPNE 507
QY	582	TLTFDGMKPKYECVKHGDYTDKAFKLCPEAGFSTQTVAAVGNRRQWDGGAPQTL 641
Db	508	TLTFDGMKPKYECVKHGDYTDKAFKLCPEAGFSTQTVAAVGNRRQWDGGAPQTL 567
QY	642	QMMAVADITSTCTGPDSESVLSVSGQEGKTK 673
Db	568	QMMAVADITSTCTGPDNQVIVIEGIPGNRK 599
RESULT 6		
ABU54635		
ID	ABU54635	standard; protein; 403 AA.
XX	AC	ABU54635;
XX	DT	03-JUN-2003 (first entry)
XX	DE	Human NOVX polypeptide #94.
XX	KW	Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
KW	KW	hypertension; congenital heart defect; aortic stenosis; valve disease;
KW	KW	atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW	KW	pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
KW	KW	tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;
KW	KW	obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW	KW	Parkinson's disease; immune disorder; haematopoietic disorder;
KW	KW	haemophilia; hypercoagulation; Crohn's disease; cancer.
XX	OS	Homo sapiens.

XX	WO200281498-A2.	
PN	17-OCT-2002.	
XX	03-APR-2002; 2002WO-US010780.	
XX	03-APR-2001; 2001US-0281086P.	
PR	03-APR-2001; 2001US-0281136P.	
PR	05-APR-2001; 2001US-0281863P.	
PR	06-APR-2001; 2001US-0281906P.	
PR	06-APR-2001; 2001US-0282020P.	
PR	10-APR-2001; 2001US-0282930P.	
PR	10-APR-2001; 2001US-0282934P.	
PR	12-APR-2001; 2001US-028312P.	
PR	13-APR-2001; 2001US-028310P.	
PR	17-APR-2001; 2001US-0284234P.	
PR	19-APR-2001; 2001US-0285325P.	
PR	20-APR-2001; 2001US-0285381P.	
PR	20-APR-2001; 2001US-0285609P.	
PR	23-APR-2001; 2001US-0285748P.	
PR	23-APR-2001; 2001US-028590P.	
PR	24-APR-2001; 2001US-0286068P.	
PR	25-APR-2001; 2001US-0286292P.	
PR	27-APR-2001; 2001US-0287213P.	
PR	02-MAY-2001; 2001US-0288257P.	
PR	29-MAY-2001; 2001US-0294164P.	
PR	30-MAY-2001; 2001US-0294484P.	
PR	18-JUN-2001; 2001US-0298952P.	
PR	19-JUN-2001; 2001US-0299237P.	
PR	19-JUN-2001; 2001US-0299276P.	
PR	12-SEP-2001; 2001US-0318750P.	
PR	25-SEP-2001; 2001US-0324800P.	
PR	25-SEP-2001; 2001US-0324802P.	
PR	27-SEP-2001; 2001US-0325684P.	
PR	17-OCT-2001; 2001US-0330143P.	
PR	14-NOV-2001; 2001US-0332111P.	
PR	14-NOV-2001; 2001US-0332240P.	
PR	14-NOV-2001; 2001US-0332779P.	
PR	21-NOV-2001; 2001US-0332115P.	
PR	04-DEC-2001; 2001US-0337621P.	
PR	03-JAN-2002; 2002US-0345783P.	
PR	16-JAN-2002; 2002US-0350251P.	
PR	02-APR-2002; 2002US-00114270.	
XX	(CURA-) CURAGEN CORP.	
XX	Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;	
PI	Patturajan M, Liu X, Gusev VV, Li L, Vernet CAM, Zerhusen BD;	
PI	Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Garlach V;	
PI	Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji W;	
PI	Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DU;	
PI	MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;	
PI	Ellerman K;	
XX	WPI; 2003-046858/04.	
DR	N-PSDB; ABX72263.	
XX	New isolated NOVX polypeptide useful for treating atherosclerosis,	
PT	metabolic disorders, diabetes, obesity, infectious disease, anorexia,	
PT	neurodegenerative disorders, Alzheimer's disease and cancer.	
XX	Claim 1; Page 292; 666pp; English.	
PS	The invention relates to human polypeptides, termed NOVX, and the	
XX	polynucleotides encoding them. The polypeptides and polynucleotides are	
CC	useful for diagnosing disease, and screening for potential therapeutic	
CC	agents. The sequences are useful for treating metabolic disorders,	
CC	cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic	
CC	stenosis, atrial septal defect (ASD), atrioventricular canal defect,	
CC	ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular	
CC	septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,	
CC	atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative	

CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease  
CC and cancer. Sequences ABU5452-ABU54647 represent human NOVX polypeptides  
CC of the invention  
XX  
SQ Sequence 403 AA;

Query Match 58.4%; Score 2111.5; DB 6; Length 403;  
Best Local Similarity 99.0%; Pred. No. 5.6e-157;  
Matches 399; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MDKYDVIKAIGOGAFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKKEVILLKMKH 60  
DB 1 MDKYDVIKAIGOGAFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKKEVILLKMKH 60  
QY 61 PNIVAFNSFQNGRLFTIMEYCDGGDLMKRINRQGVLFSDQILGWFOISLGLKHH 120  
DB 61 PNIVAFNSFQNGRLFTIMEYCDGGDLMKRINRQGVLFSDQILGWFOISLGLKHH 120  
QY 121 DRKILHRDIKAQNIIFLSKNGMVAKLDFGIARVLNNSMELARTGIGTPYLSPEICQKP 180  
DB 121 DRKILHRDIKAQNIIFLSKNGMVAKLDFGIARVLNNSMELARTGIGTPYLSPEICQKP 180  
QY 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRELHLSLSOLF 240  
DB 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRELHLSLSOLF 240  
QY 241 QVSPDRSINSILKRPFLNLIPLYLTPV-IQEPFSHMLICRAGAPASHAGKVVQKC 299  
DB 241 QVSPDRSINSILKRPFLNLIPLYLTPVFEFEEFHSMLICRAGAPASHAGKVVQKC 300  
QY 300 KIQKVFQKCPKPPRSISVPIKRNAILHRNWRPPAGAKARSIMIERPKIAVCGHYD 359  
DB 301 KIQKVFQKCPKPPRSISVPIKRNAILHRNWRPPAGAKARSIMIERPKIAVCGHYD 360  
QY 360 YYYAQLDMLRRAHKPSVHPICQENTGVEDYQOETRHGSPSQ 402  
DB 361 YYYAQLDMLRRAHKPSVHPICQENTGVEDYQOETRHGSPSQ 403

RESULT 7  
ABU54634  
ID ABU54634 standard; protein; 399 AA.  
XX  
AC ABU54634;  
XX  
DT 03-JUN-2003 (first entry)  
XX  
DE Human NOVX polypeptide #93.  
XX  
KW Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;  
KW hypertension; congenital heart defect; aortic stenosis; valve disease;  
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;  
KW tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;  
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;  
KW Parkinson's disease; immune disorder; haematopoietic disorder;  
KW haemophilia; hypercoagulation; Crohn's disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WC020281498-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002MO-US010780.  
XX  
PR 03-APR-2001; 2001US-0281086P.  
PR 05-APR-2001; 2001US-0281136P.  
PR 05-APR-2001; 2001US-0281863P.  
PR 05-APR-2001; 2001US-0281904P.  
PR 06-APR-2001; 2001US-0282028P.  
PR 10-APR-2001; 2001US-0282930P.

PR 10-APR-2001; 2001US-0282934P.  
PR 12-APR-2001; 2001US-0283512P.  
PR 13-APR-2001; 2001US-0283710P.  
PR 17-APR-2001; 2001US-0284234P.  
PR 19-APR-2001; 2001US-0285325P.  
PR 20-APR-2001; 2001US-0285381P.  
PR 20-APR-2001; 2001US-0285609P.  
PR 23-APR-2001; 2001US-0285748P.  
PR 23-APR-2001; 2001US-0285890P.  
PR 24-APR-2001; 2001US-0286068P.  
PR 25-APR-2001; 2001US-0286292P.  
PR 27-APR-2001; 2001US-0287213P.  
PR 02-MAY-2001; 2001US-0288257P.  
PR 29-MAY-2001; 2001US-0294164P.  
PR 30-MAY-2001; 2001US-0294484P.  
PR 18-JUN-2001; 2001US-0298952P.  
PR 19-JUN-2001; 2001US-0299237P.  
PR 19-JUN-2001; 2001US-0299276P.  
PR 12-SEP-2001; 2001US-0318750P.  
PR 25-SEP-2001; 2001US-0324800P.  
PR 25-SEP-2001; 2001US-0324802P.  
PR 27-SEP-2001; 2001US-0325684P.  
PR 17-OCT-2001; 2001US-0330143P.  
PR 14-NOV-2001; 2001US-0332131P.  
PR 14-NOV-2001; 2001US-0332240P.  
PR 21-NOV-2001; 2001US-0332779P.  
PR 04-DEC-2001; 2001US-0332115P.  
PR 03-JAN-2002; 2002US-0345783P.  
PR 16-JAN-2002; 2002US-0350251P.  
PR 02-APR-2002; 2002US-00114270.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;  
PI Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerkhusen BD;  
PI Gorman L, Shency SG, Pena CE, Smithson G, Burgess CE, Gerlach V;  
PI Padigaru M, Shimkets RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W;  
PI Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;  
PI Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;  
PI Ellerman K;  
XX  
XX WPI; 2003-046858/04.  
DR N-PSDB; ABX72262.  
XX  
XX New isolated NOVX polypeptide useful for treating atherosclerosis,  
PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,  
PT neurodegenerative disorders, Alzheimer's disease and cancer.  
XX  
XX Claim 1; Page 291; 666pp; English.  
XX  
XX The invention relates to human polypeptides, termed NOVX, and the  
CC polynucleotides encoding them. The polypeptides and polynucleotides are  
CC useful for diagnosing disease, and screening for potential therapeutic  
CC agents. The sequences are useful for treating metabolic disorders,  
CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic  
CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,  
CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular  
CC septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,  
CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative  
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease  
CC and cancer. Sequences ABU5452-ABU54647 represent human NOVX polypeptides  
CC of the invention  
XX  
XX Sequence 399 AA;  
SQ  
Query Match 58.3%; Score 2106.5; DB 6; Length 399;  
Best Local Similarity 99.3%; Pred. No. 1.4e-156;  
Matches 399; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 1 MDKYDVIKAIGOGAFKAYLAKGSDSKHCVIKKEINFEKMPIQKEASKKEVILLKMKH 60



AC AAO26613;  
 XX 28-MAR-2003 (first entry)  
 XX Serine/threonine protein kinase-like enzyme related mouse protein.  
 XX Cytostatic; antiparkinsonian; nootropic; neuroprotective; cardiant;  
 KW hypotensive; antiarrhythmic; antianal; analgesic; antiinflammatory;  
 KW antidiabetic; tranquilizer; antimanic; antidepressant; uropathic;  
 KW anorectic; serine/threonine protein kinase; enzyme; cancer;  
 KW central nervous system disorder; cardiovascular disorder; diabetes;  
 KW chronic obstructive pulmonary disease; obesity; genito-urinary system;  
 KW pain; genetic testing; mouse.  
 XX Mus musculus.  
 OS WO200299096-A1.  
 PN 12-DEC-2002.  
 PD 06-JUN-2002; 2002WO-EP006203.  
 XX 07-JUN-2001; 2001US-0296164P.  
 PR 19-SEP-2001; 2001US-0323100P.  
 PR 25-OCT-2001; 2001US-0330578P.  
 PR 17-JAN-2002; 2002US-0348601P.  
 XX (FARB ) BAYER AG.  
 PA Smolyar A, Horner EJ, Thelwell C;  
 PI WPI; 2003-140620/13.  
 XX New human serine/threonine protein kinase-like enzyme polypeptide and  
 PT polynucleotide, useful for regulating the activity of the protein kinase-  
 PT like enzyme to prevent, treat or ameliorate diabetes, cancer or obesity.  
 PS Disclosure; Fig 3; 157pp; English.  
 XX The invention relates to an isolated polynucleotide comprising: a  
 CC polynucleotide encoding a serine/threonine protein kinase-like enzyme  
 CC polypeptide; a sequence of 840, 990, 1120, 2142, or 1383 base pairs fully  
 CC defined in the specification; a polynucleotide that hybridizes to the  
 CC serine/threonine protein kinase-like enzyme DNA or a fragment thereof; or  
 CC a degenerate analogue of the said polynucleotides. The serine/threonine  
 CC protein kinase-like enzyme polypeptide and polynucleotide are useful in  
 CC preventing, ameliorating, or treating diseases associated with serine/  
 CC threonine protein kinase-like enzyme dysfunction such as cancer, central  
 CC nervous system disorders, cardiovascular disorders, chronic obstructive  
 CC pulmonary disease, diabetes, obesity, or disorders of the genito-urinary  
 CC system. These can also be used to treat pain associated with the above  
 CC disorders. The serine/threonine protein kinase-like enzyme polypeptide is  
 CC also useful in diagnostic assays or in genetic testing. The expression  
 CC vector or the reagent is useful in preparing a medicament for modulating  
 CC the activity of a serine/threonine protein kinase-like enzyme in a  
 CC disease, e.g. cardiovascular disorder, obesity, a disorder of the genito-  
 CC urinary system, a central nervous system disorder, diabetes, cancer, or  
 CC chronic obstructive pulmonary disease. The methods are useful in  
 CC producing and detecting the polynucleotide and polypeptide and in  
 CC screening for agents that modulate the activity of the serine/threonine  
 CC protein kinase-like enzyme polypeptide. This sequence represents a mouse  
 CC protein relating to the the serine/threonine protein kinase-like enzyme  
 CC of the invention  
 XX Sequence 774 AA;  
 SQ Query Match 30.6%; Score 1106.5; DB 6; Length 774;  
 Best Local Similarity 35.2%; Pred. No. 1e-77;  
 Matches 276; Conservative 121; Mismatches 207; Indels 181; Gaps 23;  
 1 MDKYDVIKAIGQAFKAYLAKGSDSKHCVKEINFEKMPIQEAKSKVEVILLERKXK 60  
 1 MEKYVRLQKIGEGSFGKAVLVKSTEDGRHYVKEINISRMDSKGRQESRREAVLVANXK 60

QY 61 PNIVAFNSFOENGRLEFIWMEYCDGGDLMKRINRQGVLFSDQILGWFWQISLGLKHH 120  
 DB 61 PNIVQYKESFEENGSLYIVMDYCEGDLFKRINAQKALFOEDQLDFWQICLAKHVV 120  
 QY 121 DRKILHRDIAKONIFLSKNGVMVKLGDGFIARVLNNSMELARTCTGTYLSPICQK 180  
 DB 121 DRKILHRDIAKONIFLSKNGVMVKLGDGFIARVLNNSMELARTCTGTYLSPICQK 179  
 QY 181 YNNKTDIWSLGCVLVELCTLKHPPFEGNNLQQLVLAICQAHFAPISPGFSREHLSISOLF 240  
 DB 180 YNNKTDIWSLGCVLVELCTLKHPPFEGNNLQQLVLAICQAHFAPISPGFSREHLSISOLF 239  
 QY 241 QVSPDRPSINSILKRPFLNLI PKYLTPEVTOEFESHMLICRAG----- 285  
 DB 240 KENPRDRPSVNSILEKGFIAKRIEKLSPQIAEELFKTSLKFGPQPLGKRPSAGGV 299  
 QY 285 -----APASRHAGKGVOKIKQVRFQKCPSPSRIS--VPIKRNAILHNEWRP 333  
 DB 300 SSFVPAQKITPAKYGVPLTYKTYGDKKLLKLEKPPPKHQAHOIPVKK--MNSGEERK 356  
 QY 334 PAG--AQKARSIMIER----- 348  
 DB 357 KMSEEAACKRRLEFIEKEKKQKQDQIRFLKAEQMKRQERQRLERINRAREQGWNVLRAGG 416  
 QY 349 -----PKIAAVCGHVDYVYQQLDLRR-RAH-----KPSVHP--IQOE 383  
 DB 417 SGEVKASFFGIGAVSPSPSPRGQVHYHAIFDQVQRLEADNEARWKGGIYGRWLPER 476  
 QY 384 NTG---VEDYGOETRHGSPSPQPAEYLQKPEAQYKLVKVE-----KQLGLRPSS 431  
 DB 477 QXGHLAVERANQ-----VEEFLQKREAMQKARAEHVYVLAARLQIRLQ--- 522  
 QY 432 APNINQROELR-----SNGEPRPQELPFRKNEMKEQYWKQLEIEIQOYHN 479  
 DB 523 ---NFNERQKIKAKULGENKEADGTGQGEAT--EETDMR---LKKMESLKAQTNABAALVK 575  
 QY 480 DMKEIRKMKGREPEENSKISHKTYLVKSNLNPVHDQASE-GEAPVQDIEKDLKQMLQNT 538  
 DB 576 EQLEKRRKAEYERKXKVMWEHLVAVKSDVPLPLELLETGSP----- 619  
 QY 539 KSKNPEQYKAKGVKPEINLDKISDENILQEEAMDIPNETLT-----FEDGMK 590  
 DB 620 --SKQGVKPIVSVTALKVEVGLDGLTD---TQEEEMKSNLSAISKREILRLNENLK 673  
 QY 591 FKYEYCVKSHGVDYDKAFPEKHLHCPAEGFSTQVAAVGNRRQWDGAPQTLQOMAVADIT 650  
 DB 674 AQEDEKEKHQ--HSGSCETVGHKDEREYETEN-AISSDRKKWEMGG-QLVPLDVAITLT 729  
 QY 651 STCPT 655  
 DB 730 SPSAT 734  
 RESULT 10  
 ID ABP71711 standard; protein; 774 AA.  
 XX ABP71711;  
 AC ABP71711;  
 XX 17-APR-2003 (first entry)  
 DT NEK-like serine/threonine protein kinase NEX1\_mouse # SEQ ID 3.  
 XX NEK-like serine/threonine protein kinase; cytotostatic; cardiant;  
 KW antiinflammatory; nootropic; neuroprotective; cancer; colon cancer;  
 KW cardiovascular disorder; diabetes; COPD; CNS disorder; mouse; rat.  
 OS Mus musculus.  
 OS Rattus norvegicus.  
 XX WO2003000903-A2.  
 PN 2003000903-A2.  
 XX





CC cardiovascular disorders; central nervous system (CNS) disorders;  
CC diabetes; and chronic obstructive pulmonary disease. In particular the  
CC DNA and protein sequences of the invention are useful for treating:  
CC congestive heart failure; myocardial infarction; ischaemic heart disease;  
CC arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; and  
CC peripheral or chronic pain. The present amino acid sequence represents a  
CC human serine/threonine protein kinase NEK1-related protein  
XX  
SQ Sequence 774 AA;  
Query Match 30.6%; Score 1106.5; DB 6; Length 774;  
Best Local Similarity 35.2%; Pred. No. 1e-77;  
Matches 276; Conservative 121; Mismatches 207; Indels 181; Gaps 23;  
QY 1 MDKYDVIKAGGAFKAYLAGKSDSKHCVIKINFEKMPIQEASKEVILEKMKH 60  
DB 1 MEKYVRLQIGEGSGKAVLVKSTEDGRHYVIKINISRMDSKQESRREVAVLANKH 60  
QY 61 PNIVAFFNSFOENGRFLFIWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKH 120  
DB 61 PNIVQKESFEENGSLYIMDYCEGDLFKRINAKGALFOEDDILDFWQICLAKH 120  
QY 121 DRKILHRDIKQNIPLSKNGMVAKLGDFGIARVLNNSMELARTCIGTGYLSPICQNK 180  
DB 121 DRKILHRDIKQNIPLSKNGMVAKLGDFGIARVLNNSMELARTCIGTGYLSPICEN 179  
QY 181 YNNKTDIWSLGLVYELCTLKHPPFEGNLLQVLKIQAHPAPISPGFSRELHSLISQL 240  
DB 180 YNNKSDIWLALGCVLYELCTLKHAFAGNKNLVLIISGSPVSPHYSDRLSLLQLP 239  
QY 241 QVSPDRPSINSILKRPFLNLPKYLPEVIOEFSHMLICRAG----- 285  
DB 240 KENPRDRPSVNSILEKGFIAKRIEFLSPQIAEFCILKLSKFGPQLPGKRPASQGV 299  
QY 286 -----APASHACKVQVKCKIQKVRFGKCPSPRSIS--VPIKRNAILHRENWRP 333  
DB 300 SSVPAQKITPAKRYGVPLVYKKGDKLLEKPPKPKHQAQIPVK-----MNSGEERK 356  
QY 334 PAG--AQKARSIGMIER----- 348  
DB 357 KMSEEAARLEFTEKEKKQKQDQIRFLKABQMKRQEKQRLERINRAREQGRNVLRA 416  
QY 349 -----PKIAVCGHYDYIAQLDMLR-RAH-----KSYHP--LPQE 383  
DB 417 SGKVKASFFGIGGAVSPSPSPGQYEHYHAFDMQRLRAEDNEARWKGIGYGRWLPR 476  
QY 384 NTG---VEDYQETRHGSPSPQWPAEYLQKFEAQYKLVKVE-----KQLGLRPS 431  
DB 477 QKGLHVAERANQ-----VEEFLQKREANQKARAGHVVLARLQIRLQ--- 522  
QY 432 AEPNYNQOEIR-----SNGDEPRFQELPRFNEMKQETWVKLEBEIRQOYHN 479  
DB 523 ---NFERQQIKAKLRGENEADGTGQEAT--EETDMR---LKKVESLKAQTNAARAVLK 575  
QY 480 DMKEIRKMGREPEENSKIHKTVLKKSNLPVHODASE--GEAPVDIEKDLKOMRLQNT 538  
DB 576 EQLERKREAEVEREKVWEHLVARVKSVDPLLELLEGGSP----- 619  
QY 539 KESKNPEQYKAKGVKFEINLDCISDENILQISEAMIDIPNEYLT-----FEGMK 590  
DB 620 --SKQVFPVSVTSALKEVGLDGLSLTD---TOEEEMKSNISAISKREILRENLN 673  
QY 591 PKYECVCEHGDYTDKAFKELHCPBAGFSTQTVAAVGNRRQMDGAPOTLQOMAVADIT 650  
DB 674 AQEDEKEQH--HSGSCSTVGHKBEREYETEN-AISDRKKWGGG-QLVPLDVAITLDT 729  
QY 651 STCPT 655  
DB 730 SFSAT 734  
RESULT 12.  
ABP97691

ID ABP97691 standard; protein; 774 AA.  
XX ABP97691;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Amino acid sequence of human protein sharing some identity with NEK3.  
XX  
XX Human; serine threonine protein kinase; NEK3; chromosome 13q14.3; cancer;  
KW colon cancer; central nervous system disorder; mood disorder;  
KW anxiety disorder; Parkinson's disease; Alzheimer's disease;  
KW cardiovascular disorder; myocardial infarction; hypertension; arrhythmia;  
KW embolism; acute arterial thrombosis; ischaemic disease; angina pectoris;  
KW chronic obstructive pulmonary disease; diabetes; pain.  
XX  
XX Homo sapiens.  
OS  
FN WO2003000874-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 25-JUN-2002; 2002WO-EP006993.  
XX  
PR 25-JUN-2001; 2001US-0300067P.  
PR 13-NOV-2001; 2001US-0331225P.  
PR 04-DEC-2001; 2001US-0334952P.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Xiao Y;  
XX  
XX WPI; 2003-221415/21.  
XX  
XX New human serine/threonine protein kinase NEK3 polypeptide and  
PT polynucleotide, useful in preventing, ameliorating, or treating diseases  
PT associated with serine/threonine protein kinase NEK3 dysfunction such as  
PT cancer or diabetes.  
XX  
XX Disclosure; Fig 6; 14pp; English.  
XX  
XX The present sequence represents a human polypeptide, sharing some  
CC identity with a human serine/threonine protein kinase NEK3 polypeptide.  
CC The gene is located on chromosome 13q14.3. The serine/threonine protein  
CC kinase NEK3 polypeptide and polynucleotide are useful in preventing,  
CC ameliorating, or treating diseases associated with serine/threonine  
CC protein kinase NEK3 dysfunction such as cancer, particularly colon  
CC cancer, central nervous system disorders (e.g. mood disorders, anxiety  
CC disorders, Parkinson's disease or Alzheimer's disease), cardiovascular  
CC embolism, acute arterial thrombosis, ischaemic diseases or angina  
CC pectoris), chronic obstructive pulmonary disease, or diabetes. These can  
CC also be used to treat pain associated with the above disorders. The  
CC serine/threonine protein kinase NEK3 polypeptide is also useful in  
CC diagnostic assays or in genetic testing  
XX  
SQ Sequence 774 AA;  
Query Match 30.6%; Score 1106.5; DB 6; Length 774;  
Best Local Similarity 35.2%; Pred. No. 1e-77;  
Matches 276; Conservative 121; Mismatches 207; Indels 181; Gaps 23;  
QY 1 MDKYDVIKAGGAFKAYLAGKSDSKHCVIKINFEKMPIQEASKEVILEKMKH 60  
DB 1 MEKYVRLQIGEGSGKAVLVKSTEDGRHYVIKINISRMDSKQESRREVAVLANKH 60  
QY 61 PNIVAFFNSFOENGRFLFIWMEYCDGDLMKRINRQGVLFSEDOILGFWQISLGLKH 120  
DB 61 PNIVQKESFEENGSLYIMDYCEGDLFKRINAKGALFOEDDILDFWQICLAKH 120  
QY 121 DRKILHRDIKQNIPLSKNGMVAKLGDFGIARVLNNSMELARTCIGTGYLSPICQNK 180  
DB 121 DRKILHRDIKQNIPLSKNGMVAKLGDFGIARVLNNSMELARTCIGTGYLSPICEN 179



QY 181 YNNKTDIKSLGCVLYELCTLKHPPFSGNNLQOLVLKICQAHFAPISPGFSLHSLISOLF 240  
Db 180 YNNKSDIHWALGCVLYELCTLKHAFAGNNKLVLLKISGSPFPVPHYSYDLRSLSOLF 239  
QY 241 QVSPDRPSINSILKRPFLNIPKYLTPFVIOEEFSHMLICRAG----- 285  
Db 240 KRNPRDRPSVNSILEKGFIAKRIEFLSPQLIAEEFCLTKLSKFGPQLPGKRPASGGGV 299  
QY 286 -----APASHAGKVQCKIKQVRFGKCPSPRSIS--VPIKRNAILHNEWRP 333  
Db 300 SEFVPAKIKTFAAKYGVPLTKYKYGDKLLEKPPKHOAHQIPVKK---MNSGEERK 356  
QY 334 PAG--AQKARSIMIER----- 348  
Db 357 KWSEAAKRRLEFIEKEKKQDQIRFLKAEQMKQEKQRLERINRAREQGNVLRAGG 416  
QY 349 -----PKIAVCGHYDYVYQALDMLRR-RAH-----KPSYHP--IPQE 383  
Db 417 SGFVKASFFGIGAVSPSPSPRGQYEHYHAIFDQMLRAEDNEARWKGIYGRWLPER 476  
QY 384 NTG---VEDYGGQTRHGSPSPQWPAEYLQKPEAQYKLVKVE-----KQLGLRPS 431  
Db 477 QKGLHVAERANQ-----VEEFLQKREANQKARAGHVYVYLARLQRLQ--- 522  
QY 432 AEPNVNQRQLR-----SNGEPRPQELPFRKNEMKEOBYWKQLEETRQOVHN 479  
Db 523 ---NFNERQOIKAKLGRNKEADGKGQEAT--EETDMR---LKKMESLKQAQTNAAAVLK 575  
QY 480 DMKETRKMGRPEPENSISKIHTKYLKVNKSNLPVHODASE-GEAPVDIDEKDKQMLQNT 538  
Db 576 EQLERKREAYEREKWEHVLVAVKSDVPLPLELLETGSP----- 619  
QY 539 KESKNPEQYKAKGKVFENLDKICSDENILQEEANDIPNETLT-----FEDGMK 590  
Db 620 --SKQVKPVISVTSALKVEGLDGLTD---TQEEEMKSNASISKREILRLNENLK 673  
QY 591 FKEYECVKEHGNDYDKAEKELHCPAGSPSTQTVAAVGNRQWDGCGAPQTLQMAVADIT 650  
Db 674 AQEDSEKQKH--HSGSCETVGHKDBREYETEN-AISDRKKWEMGG-QLVPLDAVTLDT 729  
QY 651 STCPT 655  
Db 730 SPSAT 734  
RESULT 13  
ID AAM39210 standard; protein; 1242 AA.  
AC AAM39210;  
XX  
DT 22-OCT-2001 (first entry)  
DE Human polypeptide SEQ ID NO 2355.  
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
OS Homo sapiens.  
XX  
FN WO200153112-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
PA (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou F, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
DR N-PSDB; AAI58366.  
XX Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.  
PS Example 4; SEQ ID NO 2355; 10078pp; English.  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 1242 AA;  
Query Match 30.6%; Score 1105.5; DB 4; Length 1242;  
Best Local Similarity 33.7%; Pred. No. 2.4e-77;  
Matches 283; Conservative 121; Mismatches 208; Indels 229; Gaps 22;  
QY 1 MDKVDVKAICGAGFAGKAYLAKGSKSKVCVKEINFEKMPIOEKEASKEVILLKMKH 60  
Db 1 MEKYVRLQKIGEGSGFKAILVKTSTEDGRQYVKEINISRMSSKERESREAVLANMKH 60  
QY 61 PNIVAFNPSFQENGRFLFVMEYCDGDLKMRINRQGVLFSEDIILGWFVQISLGLKHH 120  
Db 61 PNIVQYRESPEENGSLYVMDYCEGDLPRINAQGVLFQEDQILDWFIQICLAKHVV 120  
QY 121 DRKILHRDIKAQNIPLSKNGWAKLGDGFIARVANNMELARTICITPYLSPICQKPK 180  
Db 121 DRKILHRDIKSNIFLTQDGTV-QLGDFGIARVNSTVELARTICITPYLSPICENKP 179  
QY 181 YNNKTDIWSLGCVLVELCTLKHPPFSGNNLQOLVLKICQAHFAPISPGFSLHSLISOLF 240  
Db 180 YNNKSDIHWALGCVLYELCTLKHAFAGNNKLVLLKISGSPFPVPHYSYDLRSLSOLF 239  
QY 241 QVSPDRPSINSILKRPFLNIPKYLTPFVIOEEFSHMLICRAG---PASHAG--- 293  
Db 240 KRNPRDRPSVNSILEKGFIAKRIEFLSPQLIAEEFCLTKLSKFGSPQIPAKSPASQNS 299  
QY 294 -----KVQCKIKQVRFGKCPSPRSISVPIKRNAI 325  
Db 300 ISVNPQAKITKPAKYGIPLAYKYGDKLLEKPPKHOAHQIPVKK---WRPPAGAQA 340  
QY 326 -----LHRNE----- 358  
Db 359 SEEAARKERLEFIEKEKKQDQIRFLKAEQMKQEKQRLERINRAREQGNVLRAGG 418  
QY 341 RSIKX-----IERPKIAAVCGHYDYVYQALDMLRRRAKPSYHPIPDQENTGVEDYG-- 391

Db 419 GEVKAPFLGSGGTIAPSSFRGQYEHYHAIFDQMQQRAEDN-----EAKWKREIYGRG 473  
 QY 392 ----QETRHGSPSPQWPAEYLQKFEAQYKLVKQKQLG-----RPSSAEPNPN 437  
 Db 474 LPERQKQLAVERAKQVEEFLQKREAMQKARAEHGMILQNLAAVMYGGPSS-----527  
 QY 438 QRQELRSNGEPRFOELPRKNEMKEQYWKQLEIRQYHNDMKEIRKQM-----488  
 Db 528 ----SRGKPRNKE-----EVLARLQIRLQNFNERQQLKALRGKKEANH 572  
 QY 489 --GREPEENSKISHKTYLVKSNLFPVHDASEGEAPVQDIEKDLQKMLQNTKESKNEPQ 546  
 Db 573 SEGQSGSEADMRK-----KTESLKAHANA---RAAV--LKEQLERKKEAYEREKVVWE 623  
 QY 547 KYKAKKGVKF-----EINLKCISDENILOEE- 573  
 Db 624 EHLVAKGVKSDVSPPLQGHETGGSPSQQWRSVISVTSALKKEGVDSLSLDTRETSEEM 683  
 QY 574 ----EAMDIPNETLTFEDGMKFKE-----YECVKEHGYD- 605  
 Db 684 QKTNNAISSKREILRLNENLKAQDEKQKQNLSDTFEINVHEDAKEHEKESVSDRKK 743  
 QY 606 -KAFELKHP-----EAGFSTQTVAAVGN-----PROWDGAPQTLQMAVAD 648  
 Db 744 WEAGQQLVPLDELTLDT7SFSTTERHTVGEVILKGPNGSPRAWGKSPTDSVLKILGEAE 803  
 QY 649 I 649  
 Db 804 L 804  
 RESULT 14  
 AAO16440  
 ID AAO16440 standard; protein; 1242 AA.  
 XX AC AAO16440;  
 XX DT 10-APR-2003 (first entry)  
 XX DE Human serine/threonine protein kinase NEK1.  
 XX KW Human; gene therapy; serine/threonine protein kinase; NEK1; cancer;  
 KW colon cancer; cardiovascular disorder; congestive heart failure;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;  
 KW CNS disorder; diabetes; myocardial infarction; ischaemic heart disease;  
 KW arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease;  
 KW peripheral pain; chronic pain.  
 XX OS Homo sapiens.  
 XX PN WO2003000873-A2.  
 XX PD 03-JAN-2003.  
 XX PF 21-JUN-2002; 2002WO-EP006879.  
 XX PR 25-JUN-2001; 2001US-0300071P.  
 XX PR 16-NOV-2001; 2001US-0331447P.  
 XX PR 07-DEC-2001; 2001US-0336693P.  
 XX PA (FARB ) BAYER AG.  
 XX PI Xiao Y;  
 XX DR WPI; 2003-201424/19.  
 XX DR N-PSDB; AAL51590.  
 XX PT New serine/threonine protein kinase NEK1 gene and protein, useful for  
 PT identifying modulators of serine/threonine protein kinase NEK1 activity,  
 PT and in gene therapy for treating cancer, diabetes, heart failure or  
 PT Alzheimer's disease.  
 XX PS Claim 1; Fig 2; 156pp; English.

XX The invention comprises the amino acid and coding sequence of the human  
 CC serine/threonine protein kinase NEK1. The DNA and protein sequences of  
 CC the invention are useful for modulating the activity of serine/threonine  
 CC kinase NEK1 in a disease, such as: cancer (particularly colon cancer);  
 CC cardiovascular disorders; central nervous system (CNS) disorders;  
 CC diabetes; and chronic obstructive pulmonary disease. In particular the  
 CC DNA and protein sequences of the invention are useful for treating:  
 CC congestive heart failure; myocardial infarction; ischaemic heart disease;  
 CC arrhythmia; hypertensive; Alzheimer's disease; Parkinson's disease; and  
 CC peripheral or chronic pain. The present amino acid sequence represents  
 CC the human serine/threonine protein kinase NEK1 of the invention  
 XX Sequence 1242 AA;  
 SQ  
 Query Match 30.6%; Score 1105.5; DB 6; Length 1242;  
 Best Local Similarity 33.7%; Pred. No. 2.4e-77;  
 Matches 283; Conservative 121; Mismatches 208; Indels 229; Gaps 22;  
 QY 1 MDKYDVIKAGGATGATGAYLAKGSDSKHCVIKENFEKMPQIEKXKKEVILLERKMH 60  
 Db 1 MEKYVRLQKIGSGTGKAILVASTEDGRQYVIKEINISMSKEREESRREVAVLANMKH 60  
 QY 61 PNIVAFNFSQNGRLFIWMEYCDGDLMKRINRGVLFSEDDQLGWFWQISLGLKHH 120  
 Db 61 PNIVQRESFEENGLIYMDYCEGGDLFKRINAGKGVLFQEDQLDWFVQICLAKHVV 120  
 QY 121 DRKILHRDIKAONIFLSKNGVAKLGDGFIARVLNLSMELARTCIGTPYILSPETCNKP 180  
 Db 121 DRKILHRDIKSONIFLTQDGV-QLGDFGIARVLNSTVELARTCIGTPYILSPETCNKP 179  
 QY 181 YNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVKICQAHFAPISPGFSRELHSLISQLF 240  
 Db 180 YNKSIDIWALGCVLYELCTLKHAPEAGSMKNLVLIISGSPFVPSLHYSYDLRLSVLSQLF 239  
 QY 241 QVSPDRPSINSILKRPLENLIPKYLTPVIOEFPESHMLICRAGA---PASRHAG----293  
 Db 240 KENPRDRPSVNSILEKGFIAKRIEKLSPQIAEFCILTKFSKFGSPIPAKRPASGQNS 299  
 QY 294 ----KWQCKIKQVRFQKCPPRSISVPIKRNAI 325  
 Db 300 ISVMPAQKITKPAKYGIPLAVKYGDKLEHKKPLQKHK-QAHTPEKRYNTGEERKI 358  
 QY 326 ----LHRNE-----WRPAGAOKA 340  
 Db 359 SEEAARKRLLETFIEKKQKQDIIISLMKAEQMKQEKERLERINRARBQGRNVLSAGS 418  
 QY 341 RSIKM-----IERPKIAAVCGHYDYVAOLDMLRRRAHKPSVHPHQENTGVEDYG--391  
 Db 419 GEVKAPFLGSGGTIAPSSFRGQYEHYHAIFDQMQQRAEDN-----EAKWKREIYGRG 473  
 QY 392 ----QETRHGSPSPQWPAEYLQKFEAQYKLVKQKQLG-----RPSSAEPNPN 437  
 Db 474 LPERQKQLAVERAKQVEEFLQKREAMQKARAEHGMILQNLAAVMYGGPSS-----527  
 QY 438 QRQELRSNGEPRFOELPRKNEMKEQYWKQLEIRQYHNDMKEIRKQM-----488  
 Db 528 ----SRGKPRNKE-----EVLARLQIRLQNFNERQQLKALRGKKEANH 572  
 QY 489 --GREPEENSKISHKTYLVKSNLFPVHDASEGEAPVQDIEKDLQKMLQNTKESKNEPQ 546  
 Db 573 SEGQSGSEADMRK-----KTESLKAHANA---RAAV--LKEQLERKKEAYEREKVVWE 623  
 QY 547 KYKAKKGVKF-----EINLKCISDENILOEE- 573  
 Db 624 EHLVAKGVKSDVSPPLQGHETGGSPSQQWRSVISVTSALKKEGVDSLSLDTRETSEEM 683  
 QY 574 ----EAMDIPNETLTFEDGMKFKE-----YECVKEHGYD- 605  
 Db 684 QKTNNAISSKREILRLNENLKAQDEKQKQNLSDTFEINVHEDAKEHEKESVSDRKK 743  
 QY 606 -KAFELKHP-----EAGFSTQTVAAVGN-----PROWDGAPQTLQMAVAD 648

Db 744 WEAGQGLVPLDELTDTSFSTERTHTVGEVILKGPNGSPRAWGKSPDTSVLKILGEAE 803  
Qy 649 I 649  
Db 804 L 804  
RESULT 15  
ID AAU07102  
AC AAU07102; protein; 1214 AA.  
XX  
XX  
DT 24-OCT-2001 (first entry)  
XX  
XX Human novel human protein, NHP #2.  
XX Human; novel human protein; NHP; breast cancer; prostate cancer;  
KW immunogen; antibody; Gene therapy; antisense.  
XX  
XX Homo sapiens.  
XX  
XX WO200161016-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 15-FEB-2001; 2001WO-US0053356.  
XX  
XX 18-FEB-2000; 2000US-0183582P.  
XX 22-FEB-2000; 2000US-0184014P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX PI Walke DW, Hu Y, Nepomnichy B, Turner CA, Zambrowicz B;  
XX  
XX WPI; 2001-502793/55.  
XX N-PSDB; AAS11558.  
XX  
XX Isolated nucleic acids encoding novel human proteins useful for the  
PT treatment of disease and as probes for testing and detection.  
XX  
XX Claim 4; Page 37-39; 69pp; English.  
XX  
XX The invention relates to novel human proteins (NHP) and the nucleic acids  
CC encoding them. The nucleic acids encode mammalian transporter proteins  
CC and are useful for the treatment (e.g. by gene therapy or antisense  
CC technology) of any of a wide variety of symptoms associated with  
CC biological disorders (e.g. breast and prostate cancer) or imbalances and  
CC as probes for the identification, selection and validation of novel  
CC molecular targets for drug discovery. The proteins may be used to raise  
CC anti-NHP antibodies. The present sequence represents an NHP of the  
CC invention  
XX  
XX Sequence 1214 AA;

Query Match 29.9%; Score 1081.5; DB 4; Length 1214;  
Best Local Similarity 34.4%; Pred. No. 1.8e-75;  
Matches 274; Conservative 129; Mismatches 226; Indels 167; Gaps 21;  
Qy 1 MBKYDVKAIGOGAGKAYLAGKSDSKHCVIKENFEKMPIOBKEASKVILLKMKH 60  
Db 1 MEKYVRLQKIGESFGKALVKSTEDGQYVIKEINIRMSKREESRREAVLANMKH 60  
Qy 61 PNIVAFNFSQENGLFIWNEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120  
Db 61 PNIVQYRESFEENGSIYVMDYCEGGDLFKRINACKGVLFQEDQLDWFVQICLAKH 120  
Qy 121 DRKILHRDIKAONIFLSKNGWAKLGDGFIARVLNNSMELARTCIGTPYILSPICQNK 180  
Db 121 DRKILHRDIKSONIFLTQDGTV-QLGDFGIARVLNSTVELARTCIGTPYILSPICEN 179  
Qy 181 YNNKTDIWSLGVLYELCTLKHPFEGNQLQVLKICQAHFAPISPGFSPRELHLSISOLF 240

180 YNNKSDIWAJGCVLYELCTLKHAFAEGSMKNVLKIIISGFPFVSLHYSYDLRSLVSOLF 239  
241 QVSPRORPSINSILKRPFLLENLIPKYLTPRVIQEEFSHMLICRAGA---PASRHAG--- 293  
240 KRNPDRPVSNSILEKGFIAKRIEFLSPOLIAEBECLTFSGSQPTPAKBPASQONS 299  
294 -----KVQCKI QKVRFOCKPPRSHISVPIKRNAI 325  
300 ISVMPAQKITPAKYGIPLAYKKYGDKKLHEKKPLQKHK-QAHQTPKRVNTGEERRKI 358  
326 -----LHRNE-----WRPPAGAQA 340  
359 SEBAARKRLFEIEKKEKKQKQIIISLMKABQMKRQERLERINRAREQGNVLSAGGS 418  
341 RSIRM-----IERPKIAVCGHYDYAQLDMLRRRAHKPSYHPIPQENTGVEDYG-- 391  
419 GEVKAPFLGSGGTIAPSSPSRGQYEHYHAI PQMOQQAEDN-----EAKWKEIYVGRG 473  
392 -----QETRHGSPSPQWPAEYLQKFAQYKLVKVE-----KQLGLRPPSAEPNYNQ 438  
474 LPERQGLAVERAKQVEEFLOKREAMQNKARAEHGMVYLARLQIRLQ-----NFNE 527  
439 RQELRS--NGEERPFQELPFRKNEMKEQYWKQLEBIRQOYHND---MKEIRKMGREPE 493  
528 RQIKAKLRGEKKEANHSEGESEBADMRRKKIESLKAHANARAVALKEQLERKKEAY 587  
494 ENSKISHKTYLVKKS-----NLPVQDASEGEAPVQ-----DIEKDLKQM-----RLQN 537  
588 EREKKVWEHLVAKGVKSDVSPPLQGHETGSGSPSKQMRSVISVTSALKEVGVDLSLTD 647  
538 TKESKNPEQK---YKAKGVKFEINLDKICISDENILQEEBEMDIPNETLTFEDGMKFKE 593  
648 TRETSEEMQKTNNNAISSKREILRLN-----ENLKAQDEKGMQNLSDTFFINVEDA 700  
594 YECVKEHGDYTDK----AFKELHCP-----EAGFSTQTVAAVGN-----RRQWD 633  
701 KEHEKEKSVSSDRKKWEAGGLVPLDELTDTSFSTERTHTVGEVILKGPNGSPRAWG 760  
634 GGAPQTLLOMNAVADI 649  
761 KSPTDSVLKILGEAEL 776

Search completed: October 8, 2004, 17:07:50  
Job time : 70 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2004, 17:02:16 ; Search time 52 Seconds  
(without alignments)  
4144.210 Million cell updates/sec

Title: US-09-940-921B-2  
Perfect score: 3616  
Sequence: 1 MDKVDVIRKAGGAFKAYL.....SVSRQEGTKDPYSPVLILM 693

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.25.\*

```

1: sp_archea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_xvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778.5	49.2	614	11 Q8CCJ0	Q8ccj0 mus musculus
2	1778.5	49.2	627	11 Q7TSC3	Q7tsc3 mus musculus
3	1135.5	31.4	336	11 Q8C6N6	Q8c6n6 mus musculus
4	1006.5	27.8	424	11 Q8CD72	Q8cd72 mus musculus
5	986	26.7	302	11 Q8BSB6	Q8bsb6 mus musculus
6	799	22.1	489	4 Q8J023	Q8j023 homo sapien
7	797.5	22.1	509	11 Q99K72	Q99k72 mus musculus
8	695.5	19.2	849	13 Q7T299	Q7t299 brachydanio
9	675.5	18.7	1123	5 Q8GI06	Q8gi06 dictyosteli
10	617.5	17.1	555	5 Q9N9C3	Q9n9c3 leishmania
11	602	16.6	645	4 Q8RG66	Q8rg66 homo sapien
12	588	16.3	637	6 Q8WNUS	Q8wnus macaca fasc
13	584	16.2	482	4 Q8TBY1	Q8tby1 homo sapien
14	583	16.1	470	4 Q8NG65	Q8ng65 homo sapien
15	583	16.1	628	11 Q8C0Q4	Q8c0q4 mus musculus
16	575	15.9	579	5 Q95XQ3	Q95xq3 caenorhabdi

17	571	15.8	365	11 Q8BW62	Q8bw62 mus musculus
18	569	15.7	357	5 Q01775	Q01775 caenorhabdi
19	567.5	15.7	841	5 Q9VC32	Q9vc32 drosophila
20	566	15.7	438	11 Q8BLS6	Q8bls6 mus musculus
21	557	15.4	442	13 Q7ZVE3	Q7zve3 xenopus lae
22	554	15.3	442	13 Q9W622	Q9w622 xenopus lae
23	550.5	15.2	568	10 Q8XA66	Q8xa66 arabidopsis
24	546.5	15.1	389	13 Q9W623	Q9w623 xenopus lae
25	546	15.1	366	11 Q8BP64	Q8bp64 mus musculus
26	542	15.0	561	5 Q76134	Q76134 tetrahymena
27	540.5	14.9	443	11 Q91Z18	Q91z18 mus musculus
28	539.5	14.9	491	4 Q86XH2	Q86xh2 homo sapien
29	534.5	14.8	326	4 Q7Z634	Q7z634 homo sapien
30	534.5	14.8	384	4 Q96QN9	Q96qn9 homo sapien
31	534.5	14.8	943	10 Q94CU5	Q94cu5 oryza sativ
32	534	14.8	440	13 Q7ZUN2	Q7zun2 brachydanio
33	532	14.7	609	10 Q947T1	Q947t1 lycopersico
34	531.5	14.7	443	11 Q921N9	Q921n9 mus musculus
35	529	14.6	549	5 Q819T8	Q819t8 tetrahymena
36	528.5	14.6	416	10 Q9LT35	Q9lt35 arabidopsis
37	525	14.5	618	10 Q8S3U7	Q8s3u7 chlamydomon
38	523	14.5	555	10 Q8RXT4	Q8rxt4 arabidopsis
39	518.5	14.3	621	10 Q8SA64	Q8sa64 populus x c
40	511.5	14.1	393	11 Q91XQ1	Q91xq1 rattus norv
41	507.5	14.0	606	10 Q9CAU7	Q9cau7 arabidopsis
42	495	13.7	1057	5 Q81SD5	Q81sd5 plasmodium
43	483	13.4	356	5 Q8N3P1	Q8n3p1 paramecium
44	476	13.2	735	5 Q9W3N8	Q9w3n8 drosophila
45	475.5	13.1	299	5 Q8T755	Q8t755 brachiosteo

#### ALIGNMENTS

RESULT 1

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Q8CCJ0
ID Q8CCJ0 PRELIMINARY; PRT; 614 AA.
AC Q8CCJ0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Weakly similar to protein kinase nek1.
GN B049667.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK032672; BAC27980.1; ..
DR MGD; MGI:12142824; B0049667.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; I.
DR PRINTS; PR00109; TYRKINASE..
DR ProDom; PD0000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

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DR PROSITE; P300108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 614 AA; 70032 MW; DA95120EA45D71BC CRC64;

Query Match
Best Local Similarity 49.2%; Score 1778.5; DB 11; Length 614;
Matches 366; Conservative 55; Mismatches 79; Indels 177; Gaps 8;

QY 1 MDKYDVIRKAGCGAGKAYLAKGKSDSKHCVTKEINFEKMPITQKEASKKEVILLKMKH 60
DB 1 MDNFHLIKIIGSTGKVKYLAQKXSESSHCVTKEISLTG-----EKEASKNEVILLARMEH 56

QY 61 PNIVAFNSFQNGRLFIWVEYCDGDDLMKRNORGVLFSEDDQLGFWQISLGLKHIH 120
DB 57 PNIVTFSSFQNGRLFIWVEYCDGDDLMQRIQORGVMFSEDDQLGFWQISLGLKHIH 116

QY 241 QVSPDRPSINSILKRPFLNIPKYLTPETVQEBFESHMLICRAGAPASRHAGKVQCK 300
DB 237 RVSPQDRPSVTLKRPFLNIPKYLTPETVQEBFESHMLICRAGAPASRHAGKVQCK 267

QY 301 IQKVRFGQKCPPRSIRISVPIKENAILHRNEWPPAGAKARSIRMIERPKIAAVCGHYD 360
DB 268 -----CSR----- 271

QY 361 YYAQLDMLRRRAHKPSYHPIPOENTGVEDYGOETRHGFS-----SQWPAEYLQKFEAQ 416
DB 272 -----IQSHAH-----MENNAI-----GPTACWRVSPWSAAVYLQKFEAQ 307

QY 417 YKLKVEKQGLRPPSSAEPNYNORQLRNGEPRFQELPFRKNEMKEQYWKQLEEEIQ 476
DB 308 YKLKVERQLGLRPPSSVEPHNPEGKQLQSHWEETKFEQLQYRKNKMKQYWKQLEEEIQ 367

QY 477 YHNDMKEIRKMGREPEENSISKSHKTYLVKKNLPHVDASEGEAPVODIEKDLQKMLQ 536
DB 368 YHNDMKEIRKMGRE----- 382

QY 537 NTKESKNPEQKYAKGVKVFENLQKICSDENILOEEEMDIPNETLTFEDGMKEVEEC 596
DB 383 -----LKEVVKFEISLQKICSEEDTVQENEAVDKLNATLSFEDGTKEQEHRC 429

QY 597 VKEHGYTDKAFKELHCHPCPAGESTQTVAAVGNRRQWDGAPOTLLQMAVADITSTCTPTG 656
DB 597 VKEHGYTDKAFKELHCHPCPAGESTQTVAAVGNRRQWDGAPOTLLQMAVADITSTCTPTG 656

RESULT 2
Q7TSC3 PRELIMINARY; PRT; 627 AA.
AC Q7TSC3,
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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DB 357 KMSEBAKRRLEFIEKEK 375
RESULT 5
Q8BSB6 PRELIMINARY; PRT; 302 AA.
AC Q8BSB6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE NIMA.
GN NEK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK034754; BAC28822.1; -.
DR MGD; MGI:97303; Nek1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 302 AA; 34328 MW; 6D5B14D7809CEB341 CRC64;

Query Match 26.7%; Score 966; DB 11; Length 302;
Best Local Similarity 62.4%; Pred. No. 9.5e-55;
Matches 181; Conservative 47; Mismatches 60; Indels 2; Gaps 2;

QY 1 MDKYDVIKAGGAFKAYLAGKSDSKHCIVKEINFEKMPIQEKEASKEVILLERKMH 60
DB 1 MEKYVRLQIGSGFGKAVLVKSTEDGRHYVYKEINISRMDSKQERQSRREAVLANKH 60
QY 61 PNIVAFNSFQNGRLFIWMEYCDGDLMKRINRGVLFSDQILGWVFOISLGLKH 120
DB 61 PNIVQKSFENGSLYVMDYCEGDLFKRINAGKGLFQEDQILWVFOICLAKKHV 120
QY 121 DRKILHRDIKAGNIFLSKNGMWAKLGDGFIARVLNNSMELARTCIGTPYLSPEICQNK 180
DB 121 DRKILHRDIKSNIFLTQDGTV-QLGDFGIARVLNSTVELARTCIGTPYLSPEICENKP 179
QY 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLOQLVKIQAHFAPISPGFSRELHLSIQLF 240
DB 180 YNNKSDIWSLGCVLVELCTLKHAFAGNKNLVKILSGSPFPSPHYSDLRSLLSQLF 239
QY 241 QVSPDRPSINSILKRPFLNIPKYLTPVEIQEFSHMLICRACAPASR 290
DB 240 KRNPRDRPSVNSILEKGIKRIEFLSPQVC-VTLPLTLNCKVLVPKTR 288

RESULT 6
Q80023 PRELIMINARY; PRT; 489 AA.
AC Q80023;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE NIMA-related protein kinase 3.
GN NEK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura M., Okano Y.;
RT "Molecular cloning of human NEK3.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072828; BAC15599.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 489 AA; 55963 MW; FAB5DAAC01EFA88A CRC64;

Query Match 22.1%; Score 799; DB 4; Length 489;
Best Local Similarity 54.0%; Pred. No. 1.1e-43;
Matches 148; Conservative 51; Mismatches 73; Indels 2; Gaps 2;

QY 1 MDKYDVIKAGGAFKAYLAGKSDSKHCIVKEINFEKMPIQEKEASKEVILLERKMH 60
DB 1 MDYVYLRMIGEGFGFGRALLVQHESSNQMFAMKEIRLPK-SFSNTQNSRKEAVLLAKKH 59
QY 61 PNIVAFNSFQNGRLFIWMEYCDGDLMKRINRGVLFSDQILGWVFOISLGLKH 120
DB 60 PNIVAFKSFEGHLYVMEYCDGDLQKQKQKGLFPEDMLNFTQCLGVNHH 119
QY 121 DRKILHRDIKAGNIFLSKNGMWAKLGDGFIARVLNNSMELARTCIGTPYLSPEICQNK 180
DB 120 KKEVLRDIKSNIFLTQNGKV-KLGDGFSARLLSNPMFACTVYVTPYVPEIWENLP 178
QY 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLOQLVKIQAHFAPISPGFSRELHLSIQLF 240
DB 179 YNNKSDIWSLGCVLVELCTLKHFFQANSWKNLVKQCGCISPLSPSHVSYELQFLVKQMF 238
QY 241 QVSPDRPSINSILKRPFLNIPKYLTPVEIQE 274
DB 239 KRNPSRPSATLLSRGIVARLVQKLPPEIINE 272

RESULT 7
Q99K72 PRELIMINARY; PRT; 509 AA.
AC Q99K72;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to NIMA (never in mitosis gene a)-related expressed kinase 3.
GN NEK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; BC005411; AA05411.1; -.  
 DR HSSP; O63450; 1A06  
 DR MGD; MG1:1344371; Nek3.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 KW SEQUENCE 509 AA; 57109 MW; 333585D0588868A1 CRC64;  
 SQ  
 Query Match 22.1%; Score 797.5; DB 11; Length 509;  
 Best Local Similarity 32.7%; Pred. No. 1.5e-43;  
 Matches 201; Conservative 100; Mismatches 187; Indels 127; Gaps 17;  
 QY 1 MDKYDVIRKAIQGFAGKAYLAKGSDSKHCVIKIEINFEKMPIQEAKSKVILLKMKH 60  
 DB 1 MDNYTVLRVIGGSGRALLVLQESSNQTFAKKEIRLKK---SDQTSTKKAIVLLAKMKH 57  
 QY 61 PNIVAFNSFQENGLFIVMEYCDGDLMKRINRGVLFSEDTQLGFWFVQISLGLKHIH 120  
 DB 58 PNIVAFKESFEAGLYIVMEYCDGDLMKRIKQKGLFPEDTILNWFQICLGVNHIH 117  
 QY 121 DRKILHRDIKAONIFLSKNGVMKAGLDFGIARVLNNSMELARTCIGTPYVLSPEICQNK 180  
 DB 118 KRVLRHLRIKSNVLETHNGKV-KLGDGSGARLLSPNPAFACTVVGTPYVPPPEIWNLP 176  
 QY 181 YNNKTDIWSLGLVVELCTLKHPPFGNNLQOLVLKICQAHFAP:SPGFSRELHSLISOLF 240  
 DB 177 YNNKSDIWSLGLVVELCALKHPFOANSWNKLLKICQGPITHPLPALYSCKLQDLVKQML 236  
 QY 241 QVSPDRPSINSILKRPPELNIPLYLTPEVIOEFESHMLICRAGAPASRAGKVQCK 300  
 DB 237 KNPSPHRSFVTLKCRGSLAPLVKCLPPIRE-----YGEQILDEIK 280  
 QY 301 IQKVAFOGKCPSPRSISVPIKENAILHNEWRNPAGAKARSIKMIERPKIAAVCGHYDY 360  
 DB 281 ISTPKMKK-----QDSNRVGEALGEANSASMQEER-GRKCSHTEL 321  
 QY 361 YQAQLDMLRRRAKHSYHPIPOENTGV-----EDYQETRHGSPSPQWPAEVLQKRFQAQ 416  
 DB 322 -----ESTGTPPAGNALGRAARGNPGN---PQEHGRHTSPASP 356  
 QY 417 YKLKVEKQLGLRPSAEPNPNQORQLRNGEPRFOELPPRKNEKMEQYWKQLLELRQ 476  
 DB 357 HRPVRERH---GPSNVEALEKASILTSS-----FTAEDRGGSVIKIYENARRQ 403  
 QY 477 YNDMMKTRKMGREPEENSKISHYTVLVKSNL-----PVHQDASGEAPVDIEKDL 530  
 DB 404 WYREPEALLSMLKADALSQ--AFQTYTYIRPGAEGFLKGLPSLSDTAS-----DSVGDGL 456  
 QY 531 KOMRLQNTKESKNPEQYKAKGVKFEINLQKCI-SDENILOEEAAMDIPNLTFLFEDGMK 590  
 DB 457 DSVML-----DPE-----RFEPRLDE--EDTDFEEDNPNPWLS----- 489

QY 591 FKEYECVKEHGHDYTD 605  
 DB 490 -----LKGVGVGD 498  
 RESULT 8  
 QY 7299 PRELIMINARY; PRT; 849 AA.  
 ID QY7299;  
 AC QY7299;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC054633; AAH54633.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 849 AA; 95966 MW; E4E8B117A0147D7B CRC64;  
 Query Match 19.2%; Score 695.5; DB 13; Length 849;  
 Best Local Similarity 27.2%; Pred. No. 1.1e-36;  
 Matches 206; Conservative 131; Mismatches 280; Indels 139; Gaps 23;  
 QY 1 MDKYDVIRKAIQGFAGKAYLAKGSDSKHCVIKIEINFEKMPIQEAKSKVILLKMKH 60  
 DB 1 MDGYLFRVVVVGXSGYGEVNLVRHKSQRKQYVTKKLNLRSSRRERRAAQEAQLLSQLKH 60  
 QY 61 PNIVAFNSFQ-ENGLFIVMEYCDGDLMKRINRGVLFSEDTQLGFWFVQISLGLKHI 119  
 DB 61 PNIVAFNSFQ-ENGLFIVMEYCDGDLMKRINRGVLFSEDTQLGFWFVQISLGLKHI 119  
 QY 120 HDRKILHRDIKAONIFLSKNGVMKAGLDFGIARVLNNSMELARTCIGTPYVLSPEICQNK 179  
 DB 121 HDRKILHRDIKAONIFLSKNGVMKAGLDFGIARVLNNSMELARTCIGTPYVLSPEICQNK 179  
 QY 180 PYNKTDIWSLGLVVELCTLKHPPFGNNLQOLVLKICQAHFAP:SPGFSRELHSLISOLF 239  
 DB 180 PYNKTDIWSLGLVVELCTLKHPPFGNNLQOLVLKICQAHFAP:SPGFSRELHSLISOLF 239  
 QY 180 PYNKTDIWSLGLVVELCTLKHPPFGNNLQOLVLKICQAHFAP:SPGFSRELHSLISOLF 239  
 DB 180 PYNKTDIWSLGLVVELCTLKHPPFGNNLQOLVLKICQAHFAP:SPGFSRELHSLISOLF 239  
 QY 240 FQVSPDRPSINSILKRPPELNIPLYLTPEVIOEFESHMLICRAGAPASRAGKVQCK 292

Db 240 LCKPEDPDKVHLRQYIKHQISMFL--BATKEKTAKRKXKNAAGKLNAGSAGDASTKP 297  
QY 293 GKWVO-KCKIKQVRQKCPKPRSRISVPIKNAIILHRNEMPPAGAQVARSIKMIEPKI 351  
Db 298 NQVQPOQLNSSEKTCG-----KKAEEIYLNRQKPCNGAWENVAPKHHMPKS 345  
QY 352 AAVCGHYDYAAQLDMLRRRAHKPSYHPQP-ENTGVEDVQCTRHGSPSPS-----QWPA 405  
Db 346 PT-----RDIHNTGGQSIATISIDIEIQKQAKPKPKSSHQNNLPS 389  
QY 406 EYLQKFE-----AQYKLGK-----VEKQGLRPPSAEPNPNQRLRNSG----- 446  
Db 390 VSKREKEDPGAPQTHPHKQVGVGTEDKMSANASSITPKPADRTKMPNKSALDVSLD 449  
QY 447 -----EPRPQELPFRKEM-----KEQYVWQLEBEIROQYVNDKKEIKKMGREPEZ 494  
Db 450 IKDDTMKLLQAGVQDLFPYPTLHNAEQKTESQRTADNOSNAGVLKDAPTGSSTESE 509  
QY 455 NSKISHKTVLKKSLPVHQDASEGEAPVQD-----IEKDLKQVRLQNTKESKNPEQ 546  
Db 510 GSLDSTEKLLKVPVIFNEPSESPPAALSDEGRSPSSSSPSMSRQRRQKDKSODLQ 569  
QY 547 KYAKKGVKFEIN--LDKCIDENILQEE-----AMDIPNETLTFEDCMKFE 593  
Db 570 -----NGIQEKVSRPLPLPEDGNSAQDQSTPAGLSSTNKSTEQNRPLSARERRLKQ 624  
QY 594 YE-----CVKEHG-DYTDKAFELH-----CPEAGPST--QTVAAGNRRQWDGCAPO 638  
Db 625 SGENSTQAVASVRKPSQVSLDSEQIHQDCPRAATTVDITKERSKQSD----- 679  
QY 639 TLLQWMAVADITSTCTGPDSESVLSVRQEGTKYD 674  
Db 680 -----EDEC-----SSSTSTSERSEGDYRE 699

RESULT 9  
Q86106  
ID Q86106 PRELIMINARY; PRT; 1123 AA.  
AC Q86106;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to Mus musculus (Mouse). 13 days embryo male testis cDNA,  
DE RIKEN full-length enriched library, clone:6030407p11 product:NIMA  
DE (Never in mitosis gene a)-related expressed kinase 1, full insert  
DE sequence.  
OS Dictyostelium discoideum (slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
CX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=22092622; PubMed=12097910;  
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,  
RA Lehmann R., Baumann C., Parra G., April J.F., Guigo R., Kumpf K.,  
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,  
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";  
RL Nature 418:79-85(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR ENBL; AL358652; CAB94013.1; --  
DR HSP; Q00534; IBI8.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002965; P rich exten.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_kinase.  
DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PRO1217; PRICHEXTENSN.  
DR PRINTS; PRO109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00219; TYRK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 1123 AA; 120808 MW; 69DFDESE2B0A3283 CRC64;  
Query Match 18.7%; Score 675.5; DB 5; Length 1123;  
Best Local Similarity 50.7%; Pred. No. 3.1e-35;  
Matches 139; Conservative 46; Mismatches 84; Indels 5; Gaps 4;  
QY 1 MDKYVKAIGGATGKAYLAGKSDSKHCVIKENFKNPIQOEKAEKKEVILLKMKH 60  
Db 1 MDKYBEIKTIGKSGFRALVKKSDGLLLVKEINVMEMQPKERSDAMNEVLLSLD 60  
QY 61 PNIVAFFNSFQNGRLFIWMEYCDGDLMKRINRQ--RGVLFSEDIQLGWVQISLGLKH 118  
Db 61 ENHIGYDSEFLNGCLYIMEVANAGDINLEIKKTLQNKTFSEFEILLSWFSQICKALQY 120  
QY 119 IHRKILHRDIKAQNFIS-KNG-MVAKLGDGFIARVLNNSMELARTCIGTPYILSPIC 176  
Db 121 ISRNILHRDLKTONIFLSVNGDYFIKLGDFGIKILNSETSLASTVLGTYPYLSPELI 180  
QY 177 QN-KPVNKTDLWSLGCVLVETLKHPEGNLQOLVKICQAHFAPISPGFSRELHSL 235  
Db 181 QNEKGYDHKSDIWSLGCVLVETLKHAFNAANLPAVLVKILKGTYPPIPSHYSNDLENL 240  
QY 236 ISQLFQVSPDRPSINSILKRPFLENLIPKYLTP 269  
Db 241 ISSMLQIDPKNRPVNDILELFPINQYLGILPKP 274

RESULT 10  
Q9N9C3  
ID Q9N9C3 PRELIMINARY; PRT; 555 AA.  
AC Q9N9C3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE NEK-related serine/threonine-protein kinase nek1.  
GN P1408.02.  
OS Leishmania major.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
CX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,  
RA Barrell B.G.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR ENBL; AL358652; CAB94013.1; --  
DR HSP; Q00534; IBI8.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.





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Db 362 KIVEEK-----YENSRMELSRNFQQLSVDLHKEKTLKG----- 399
QY 405 AYLOKFAQYQYKLVKQGLRPSAEPNYNQQLSNGEPRFQELPFK----- 458
Db 400 ---MEBKEQPEGLRSCSPQ-----DEDERWQGRE---ESDEPTLENLPESQIPSM 448
QY 459 -----NEMKEQYWK 468
Db 449 LHELESIVEDATSDGYHGDCLNLSLDEYWK 479

RESULT 14
Q8NG65
ID Q8NG65 PRELIMINARY; PRT; 470 AA.
AC Q8NG65;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NIMA-related kinase 11S.
GN NEK11S.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noguichi K., Fukazawa H., Murakami Y., Uehara Y.;
RT "Nek11, a new member of the NIVA family of kinases, involved in DNA
RT replication and genotoxic stress responses.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071997; BAC06351.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase; 1.
SQ SEQUENCE 470 AA; 54006 MW; F52B82ED2B096FFB CRC64;

Query Match 16.1%; Score 583; DB 4; Length 470;
Best Local Similarity 27.9%; Pred. No. 1e-29;
Matches 155; Conservative 93; Mismatches 161; Indels 146; Gaps 15;

QY 3 KYDVLKAIQGAAGKAYLA---KGSKDSKHCVIKEINFEKMPIQEASKEKVEILLEKWK 59
Db 28 RYVLQKLGSGFGTVLVSDKAKRGELKVKISVGLNPNETVQANLEAQLLSKLD 87
QY 60 HPNIVAFNFSQENGRLEFIVMEYCDGDLMKRIN--RQGVLFSEDIQLGFWFQISLGLK 117
Db 88 HPAIVKFAHFVEQDNFCITTEYCEGRDLDDKIQYKQAGKIFFENQIIFQLLQVLD 147
QY 118 HHDRKILHRDIKAQNIPLSKNGMVKAGLDGFIARVANNMELARTCTGTYPYLSPEICQ 177
Db 148 YHMERILRLDKSNKVFUKNN--LLKIGDFGVSRLLMGSCDALTTLTGTTHYMSPEALK 205
QY 178 NKPYNKNTDIWSLGVLCVLPKHPFEGNNIQQVLWKICQAHFAPISGFGRSLHSLIS 237
Db 206 HOGYDTKSDIWSLACILVEMCCWNAFAGSNFLSVLKIIVEGDTSLPERYFKELNAIME 265
QY 238 QLFQVSPDRPRDINSILKRPF----LENLIPKYLTFEVIQEEFSSHMLICRAGAPASRHAG 293

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Db 266 SMLNKNPSLRPSALEIILKIPYLDQQLNLMCRY-----SEMTEKNDLDCQKEAA 315
QY 294 KVV-----QKCKIQKVRFG---KPPSRISVPIKRNAILHNRWPPAGAKARSIKVI 346
Db 316 HIINAMQRIHLQTLRALSEVQKMTPRMRLR-----KLQAADEKARKLKKI 363
QY 347 ERPIAAVCGHYDYVYLAQDLWLRRAHKPSVHPPIQENTGVEDYQGTTRHGSPSQWPAE 406
Db 364 ----- 363
QY 407 YLQKFEAQYQYKLVKQGLRPSAEPNYNQQLSNGEPRFQELPFKHEMKEQY 466
Db 364 -VEEKY-----EENSKRQQLASR--NFQQLSV--DVLHEKTH 396
QY 467 WKQLEETIRQQYHNDM-----KEIRKMGREPPENSISKHTYLVKKSNIPLVHQ-----D 515
Db 397 LKGMEEKEQPEGLRSCSPQDEDERWQGREESDEP-----TLENLPESQIPSM 448
QY 516 ASEGEAPVQDIKDL 530
Db 449 LHELESIVEDATSDL 463

RESULT 15
Q8CQ04
ID Q8CQ04 PRELIMINARY; PRT; 628 AA.
AC Q8CQ04;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to mRNA.
GN 4932416N14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030042; BAC26756.1; -.
DR MGD; MGI:2442276; 4932416N14RIK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
SQ SEQUENCE 628 AA; 71666 MW; AF8672BF80DCF271 CRC64;

Query Match 16.1%; Score 583; DB 11; Length 628;
Best Local Similarity 27.9%; Pred. No. 1.5e-29;
Matches 182; Conservative 108; Mismatches 233; Indels 130; Gaps 23;

QY 3 KYDVLKAIQGAAGKAYLA---KGSKDSKHCVIKEINFEKMPIQEASKEKVEILLEKWK 59
Db 29 RYVLQKLGSGFGTVLVSDKAKRGELKVKISVGLNPNETVQANLEAQLLSRLH 88
QY 60 HPNIVAFNFSQENGRLEFIVMEYCDGDLMKRIN--RQGVLFSEDIQLGFWFQISLGLK 117

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Db 89 HPAIVRFHAFNEQTCITTEYCEGRDLRIQIYKEAGKVFAENQIVWFQILLGVD 148  
QY 118 HIHDRKILHRDIKAQNIFLSKNGMVAKLDFGIARVLNNSMELARTCIGTPYILSPEICQ 177  
Db 149 YMHERRILHRDLKSNIFLKN--LLKIGDFVGRLLMGSCELATTLTGTHYMSPEALK 206  
QY 178 NKPYNKTDIWSLGVYELCTLKHPPFEGNNLQOLVKICOAHFAPISPSPSRHLHSLIS 237  
Db 207 HQGYDAKSDIWSLACILYEMCCLHAFAGSFLSVLNIWEGKTFSPDRYPRELTIME 266  
QY 238 QLFQVSPDRPSINSILKRPFLN---LIPKYLTPVIOEFSHMLITCRAGAPASRHAG 293  
Db 267 RMLNKSPSLRPSAADILKAPYMEEOQLLMCKY--PENTLEDKNS--VCQKEA---AHTI 319  
QY 294 KVVQK-----CKIQKRFQCKPPRSRISVPKRNAILHRNEW--RPPAGAQAARSIXMIE 347  
Db 320 NAVQKHLHLQTLQALSDTQKTPRERM-----WLRKLOAADERARLKKIA 365  
QY 348 RPKIAAVCGHYDYVYAQDMLRR---AHKPSYHPIPOENTGVEDYQETRHHGSPSQW 403  
Db 366 EE-----NYKENDKRNQALRSNNGSVHVAHLVHLDERT--LESL-----PEQSL 409  
QY 404 PA---EYLQKPE-----AQYKLVKQGLRPSSEAFPNYNQCELRNSGEEPRFOELP 455  
Db 410 PCLDLDELEPSLEDITVDLGHYEIPED-----PLVAEQYYSVDVFDSCSEDEQEEMI 463  
QY 456 FRK--NEMKEQE-----YWKQ-----LEEIRQQYHNDMKEI----- 484  
Db 464 FSEAGDTRKEESPVSRYTNQODSDTAALVGCLEHVLGYTSLDTKITINAVTMSPGMV 523  
QY 485 -----RKKMGREPEEN-SKISHKTYLVKSNLPVHODASEGEAPVQDIEKDLQOMELQN 537  
Db 524 FNSAVARTKMKMKESAVQKLGMEFF-----BEVDYLKRRQRN 563  
QY 538 TKESKNPEOKYKAKKGVKFEINLDCISDENILOEEENAMDIPNETLTFEDGMK 590  
Db 564 AREAEIWEHLETVVPRASDCFEVDQLLYFEELLTMEGKEPSLQNLPCAAQK 616

Search completed: October 8, 2004, 17:09:07  
Job time : 57 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2004, 17:06:41 ; Search time 21 Seconds  
(without alignments)  
1679.073 Million cell updates/sec

Title: US-09-940-921B-2

Perfect score: 3616

Sequence: 1 MDKYDVIKALGQAGFGKAYL.....SVSRQEGTKDPYSPVLILM 683

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pgp: \*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pgp: \*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pgp: \*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pgp: \*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pgp: \*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pgp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3081.5	85.2	640	US-09-873-404-2	Sequence 2, Appli
2	1366	29.5	616	US-09-873-404-4	Sequence 4, Appli
3	816.5	22.6	345	US-09-173-581-6	Sequence 6, Appli
4	816.5	22.6	345	US-09-420-915-6	Sequence 6, Appli
5	634	17.5	692	US-09-992-481-2	Sequence 2, Appli
6	539.5	14.9	445	US-09-167-206-2	Sequence 2, Appli
7	535.5	14.8	979	US-08-870-529-2	Sequence 2, Appli
8	535.5	14.8	979	US-09-544-794-2	Sequence 2, Appli
9	517.5	14.3	699	US-09-457-040B-18	Sequence 18, Appli
10	462.5	12.8	302	US-09-221-235-2	Sequence 2, Appli
11	462.5	12.8	302	US-09-221-928-2	Sequence 2, Appli
12	462.5	12.8	302	US-09-221-237-2	Sequence 2, Appli
13	462.5	12.8	302	US-09-221-236-2	Sequence 2, Appli
14	462.5	12.8	302	US-09-221-416-2	Sequence 2, Appli
15	462.5	12.8	302	US-09-221-415-2	Sequence 2, Appli
16	462.5	12.8	302	US-09-163-115-2	Sequence 2, Appli
17	462.5	12.8	302	US-09-221-528-2	Sequence 2, Appli
18	462.5	12.8	302	US-09-593-553-2	Sequence 2, Appli
19	462.5	12.8	302	US-09-221-237-2	Sequence 2, Appli
20	458.5	12.7	302	US-09-579-664B-9	Sequence 9, Appli
21	427	11.8	233	US-08-712-709-1	Sequence 1, Appli
22	427	11.8	233	US-09-111-444-1	Sequence 1, Appli
23	427	11.8	233	US-09-541-228-1	Sequence 1, Appli
24	417.5	11.5	647	US-09-031-563-7	Sequence 7, Appli
25	417.5	11.5	647	US-09-392-277-7	Sequence 7, Appli
26	417.5	11.5	647	US-09-258-000-7	Sequence 7, Appli
27	417.5	11.5	648	US-09-031-563-5	Sequence 5, Appli

28	417.5	11.5	648	4	US-09-392-277-5	Sequence 5, Appli
29	417.5	11.5	648	4	US-09-258-000-5	Sequence 5, Appli
30	417.5	11.5	1315	3	US-09-031-563-2	Sequence 2, Appli
31	417.5	11.5	1315	4	US-09-293-505-10	Sequence 10, Appli
32	417.5	11.5	1315	4	US-09-392-277-2	Sequence 2, Appli
33	417.5	11.5	1315	4	US-09-258-000-2	Sequence 2, Appli
34	414.5	11.5	1315	3	US-09-031-563-25	Sequence 25, Appli
35	414.5	11.5	1315	4	US-09-392-277-25	Sequence 25, Appli
36	414.5	11.5	1315	4	US-09-258-000-25	Sequence 25, Appli
37	413	11.4	293	2	US-09-049-871-1	Sequence 1, Appli
38	413	11.4	293	3	US-09-295-068-1	Sequence 1, Appli
39	405.5	11.2	260	3	US-09-031-563-24	Sequence 24, Appli
40	405.5	11.2	260	4	US-09-392-277-24	Sequence 24, Appli
41	405.5	11.2	260	4	US-09-258-000-24	Sequence 24, Appli
42	403.5	11.2	925	1	US-08-252-995D-4	Sequence 4, Appli
43	403.5	11.2	925	2	US-08-834-108-4	Sequence 4, Appli
44	395.5	10.9	1269	4	US-09-645-456A-15	Sequence 15, Appli
45	395.5	10.9	1269	4	US-09-425-324A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1  
US-09-873-404-2  
; Sequence 2, Application US/09873404  
; Patent No. 6500656  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: C1001212-CIP  
; CURRENT APPLICATION NUMBER: US/09/873,404  
; CURRENT FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 640  
; TYPE: PRT  
; ORGANISM: Human  
US-09-873-404-2

Query Match	85.2%;	Score	3081.5;	DB 4;	Length	640;			
Best Local Similarity	94.1%;	Pred. No.	9.6e-236;						
Matches	585;	Conservative	2;	Mismatches	4;	Indels	31;	Gaps	1;
Qy	1	MDKYDVIKAI	GAGFGKAYLAKGSDSKHCVKEINFEKMPLOEK	EASKEVILL	EKM	H	60		
Db	1	MDKYDVIKAI	GAGFGKAYLAKGSDSKHCVKEINFEKMPLOEK	EASKEVILL	EKM	H	60		
Qy	61	PNIVAFNSFO	ENGRFLFIWVEYCDGGDLMKRINRQGVLFSEDIILGW	FVQISLGLK	HH	I	120		
Db	61	PNIVAFNSFO	ENGRFLFIWVEYCDGGDLMKRINRQGVLFSEDIILGW	FVQISLGLK	HH	I	120		
Qy	121	DRKILHRDIA	QNIIFLSKNGWAKLDFGIARVLNNSMELARTCTGTPY	LSPEICQ	NP	180			
Db	121	DRKILHRDIA	QNIIFLSKNGWAKLDFGIARVLNNSMELARTCTGTPY	LSPEICQ	NP	180			
Qy	181	YNNKTDIWS	LGCVLYELCTLKHPPFEGNNLQQLVLKICQAHFAPIS	PGFSREH	LSLSOLF	240			
Db	181	YNNKTDIWS	LGCVLYELCTLKHPPFEGNNLQQLVLKICQAHFAPIS	PGFSREH	LSLSOLF	240			
Qy	241	QVSPDRPDS	INSTLKEPFFLENIIPKYLTPVEIQEEFSHMLICRAG	APASRHAG	KVQCK	300			
Db	241	QVSPDRPDS	INSTLKEPFFLENIIPKYLTPVEIQEEFSHMLICRAG	APASRHAG	KVQCK	300			
Qy	301	IQKVRFGKC	PPSRISVPIKRNAILHRNEMPPAGAKARSIKMIERPK	IAVCGHYD	360				
Db	301	IQKVRFGKC	PPSRISVPIKRNAILHRNEMPPAGAKARSIKMIERPK	IAVCGHYD	360				
Qy	361	YYAQLDML	RRRAKPSYHPIPOENTGVEDYQGETRGPSPQWPAEY	LQKFEAQY	KLK 420				

Db 361 YYAQLDMLRRRAHKSYSHP1PQENTGVEDYQGETRHGSPSQWPAEYLQRFKFAQQYK 420  
Qy 421 VEKQGLRPSAEPNYNQRLNSGEPFQELPFRKNEMKEQYKQLEELRQYHND 480  
Db 421 VEKQGLRPSAEPNYNQRLNSGEPFQELPFRKNEMKEQYKQLEELRQYHND 480  
Qy 481 MKEIRKMGREPEENS KISHKTYLVKSNLPVHQDASEGEAPVODIEKDLQVRLQNTKE 540  
Db 481 MKEIRKMGREPEENS KISHKTYLVKSNLPVHQDASEGEAPVODIEKDLQVRLQNTKE 509  
Qy 541 SKNPQKYKAKGVKFEINLQKISDENILOEEBAMDPNETLTFEGMKFEYECVKEH 600  
Db 510 SKNPQKYKAKGVKFEINLQKISDENILOEEBAMDPNETLTFEGMKFEYECVKEH 569  
Qy 601 GYTDKAFKHLCPAGFSTOT 622  
Db 570 GYTDKAFKHLCPAATLT 591  
RESULT 2  
US-09-873-404-4  
; Sequence 4, Application US/09873404  
; Patent No. 6500656  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001212-CIP  
; CURRENT APPLICATION NUMBER: US/09/873,404  
; CURRENT FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 616  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-873-404-4  
Query Match 29.5%; Score 1066; DB 4; Length 616;  
Best Local Similarity 38.7%; Pred. No. 4e-76;  
Matches 245; Conservative 95; Mismatches 147; Indels 146; Gaps 16;  
Qy 1 MDKYDVKAIGGAGFKAYLAKGSDSKHCVIKEINFEKMPIOEKEASKEVILLKMKH 60  
Db 1 MEKYVRLQKIGSGFKAVLVKSTEDGRHYVIKEINISMSDKESQESRREAVLANMKH 60  
Qy 61 PNIVAFNSFQNGRLFIWMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120  
Db 61 PNIVQKESFENGSLYIWMYCEGDLFKRINAQKGFALFOEDQILDWVQICLAKH 120  
Qy 121 DRKILHRDIKAONIPLSKNGMVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICONKP 180  
Db 121 DRKILHRDIKSONIFLTQDGTV-QLGDFGIARVLNSTVELARTCTGTPYLSPEICENKP 179  
Qy 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRSLHLSIQ 240  
Db 180 YNNKSDIWAIGCVLYELCTLKHAFEGAGNMNLVLIISGSPVPVSHYSYDLRSLSL 239  
Qy 241 QVSPDRPSINSILKRPFLNLI PKVLTPEVTEQEFESHMLICRAG- 285  
Db 240 KRNPRDRPSVNSILEKGFIAKIEFLSPQIAEFCLTKTSKFGPQLPKRPSAGGV 299  
Qy 286 -----APASRHAGVQKCIQVRFQKCPPRSRIIS--VPKRNAILHRNWRP 333  
Db 300 SSFVPAQKITKPAKYGVPLTKYKGDKKLEKPKPKHQAQHPVKK--MNSGERK 356  
Qy 334 PAG--AQKARSIMTER----- 348  
Db 357 KMSSEAAKRRLEFIEKEKKQKDQIRFLKABQMKFEQKQRLERINRAREQWRNVLRAG 416  
Qy 349 -----PKIAAVCGHYDYVYAAQLDMLR-RAH-----KPSYHP--IPQE 383

Db 417 SGEVKASFFGIGAVSPSPGSPRGQYEHYHALFDQMQRLEADNEARWKGLIYGRWLPER 476  
Qy 384 NTG---VEDYQGETRHGSPSQWPAEYLQRFKFAQQYKLVK- 431  
Db 477 QKGLHAVERANQ-----VEEFLQRKEAMQNKARAEHVVYLRQLRQLQ--- 522  
Qy 432 APNPNQREL- 479  
Db 523 ---NFNERQOIKAURLGENKEADGTGQFAT-BETDMR---LKKWESLKAQTNARAVALK 575  
Qy 480 DMKEIRKMGREPEENS KISHKTYLVKSNLPV 512  
Db 576 EQLEKREKAEYEREKKVWEHLVARVKSDDVPL 608  
RESULT 3  
US-09-173-581-6  
; Sequence 6, Application US/09173581A  
; Patent No. 6013455  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Gorgone, Gina  
; APPLICANT: Azimzai, Yaida  
; APPLICANT: Lu, Aina  
; TITLE OF INVENTION: Protein Kinase Homologs  
; FILE REFERENCE: PF-0614 US  
; CURRENT APPLICATION NUMBER: US/09/173,581A  
; CURRENT FILING DATE: 1998-10-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PERL Program  
; SEQ ID NO 6  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: 1567782  
US-09-173-581-6  
Query Match 22.6%; Score 816.5; DB 3; Length 345;  
Best Local Similarity 44.9%; Pred. No. 1e-56;  
Matches 173; Conservative 55; Mismatches 80; Indels 77; Gaps 6;  
Qy 1 MDKYDVKAIGGAGFKAYLAKGSDSKHCVIKEINFEKMPIOEKEASKEVILLKMKH 60  
Db 1 MEKYVRLQKIGSGFKAVLVKSTEDGRHYVIKEINISMSDKESQESRREAVLANMKH 60  
Qy 61 PNIVAFNSFQNGRLFIWMEYCDGDLMKRINRQGVLFSDQILGWVQISLGLKH 120  
Db 61 PNIVQYRESF-----EGILDWVQICLAKH 88  
Qy 121 DRKILHRDIKAONIPLSKNGMVAKLGDGFIARVLNNSMELARTCTGTPYLSPEICONKP 180  
Db 89 DRKILHRDIKSONIFLTQDGTV-QLGDFGIARVLNSTVELARTCTGTPYLSPEICENKP 147  
Qy 181 YNNKTDIWSLGCVLVELCTLKHFFEGNNLQQLVLKICQAHFAPISPGFSRSLHLSIQ 240  
Db 148 YNNKSDIWAIGCVLYELCTLKHAFEGAGNMNLVLIISGSPVPVSHYSYDLRSLSL 207  
Qy 241 QVSPDRPSINSILKRPFLNLI PKVLTPEVTEQEFESHMLICRAG- 293  
Db 208 KRNPRDRPSVNSILEKGFIAKIEFLSPQIAEFCLTKTSKFGPQLPKRPSAGGV 267  
Qy 294 -----KVQCKTIQKVRFOCKCPPRSRIISVPKRNAIL 325  
Db 268 ISVMPAQKITKPAKYGVPLTKYKGDKKLEKPKPKHQAQHPVKK--MNSGERK 326  
Qy 326 LHRNWRPAPAGAKARSIMTERPK 350



327 SEB-----AARKRLRLEFIEKDK 343

Db

US-09-420-915-6

RESULT 4

Sequence 6, Application US/09420915

Patent No. 6254947

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Tang, Y. Tom

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Guégley, Karl J.

APPLICANT: Corley, Neil C.

APPLICANT: Gorsone, Gina

APPLICANT: Azimzai, Yalda

APPLICANT: Lu, Aina

TITLE OF INVENTION: Protein Kinase Homologs

FILE REFERENCES: PF-0614 US

CURRENT APPLICATION NUMBER: US/09/420,915

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US-09/173,581

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PERL Program

SEQ ID NO 6

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: -

OTHER INFORMATION: 1567782

US-09-420-915-6

Query Match 22.8%; Score 816.5; DB 3; Length 345;

Best Local Similarity 44.9%; Pred. No. 18-56;

Matches 173; Conservative 55; Mismatches 80; Indels 77; Gaps 6;

QY 1 MDKYDVIRKAGGAFGKAYLAGKSDSKHCVIKENFEKMPIOEKEASKKEVILLENKXKH 60

DB 1 MEKYVRLQIGEGSGKALVKSSTEDGRQYVIKENISEMSKEREESREAVLANVXKH 60

QY 61 PNIVAFNFGQENGRLFIVMEYCDGDLMKRINRQGVLFSDQILGFVQISGLKXHH 120

DB 61 PNIVQYRESF-----EGILDWFVQICLALKXHV 88

QY 121 DRKILHRDIKAONIPLSKNGMVAKLDFGIARVLNNSMELARTCIGTPYVLSPICONKP 180

DB 89 DRKILHRDIKSONIFLTQGTGV-QLGDFGIARVLNSTVELARTCIGTPYVLSPICONKP 147

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 240

DB 148 YNNKSDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 207

QY 241 QVSPDRPINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGA---PASRAG--- 293

DB 208 KRNPRDRPNSVLSLEKGFATAKIEFLSPQLAEFCLTKSPKSGQIPAKRPASQNS 267

QY 294 -----KVQCKIKQVRFGCKCPPRSISVPIKNAI 325

DB 268 ISVMPAQKITPAKYGIFLAYKKGDKLHKKPLQKH-QAHQTPEKRYNTGEERRKI 326

QY 326 LHRNEWPPAGAKARSIKMIERPCK 350

DB 327 SEB-----AARKRLRLEFIEKDK 343

RESULT 5

US-09-992-481-2

Sequence 2, Application US/0992481

APPLICANT: Mathur, Brian

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. 6593125e1 Human Kinases and Polynucleotides

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0266-USA

CURRENT APPLICATION NUMBER: US/09/992,481

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: US 60/252,011

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 692

TYPE: PRT

ORGANISM: homo sapiens

US-09-992-481-2

Query Match 17.5%; Score 634; DB 4; Length 692;

Best Local Similarity 38.9%; Pred. No. 7.6e-42;

Matches 147; Conservative 63; Mismatches 128; Indels 40; Gaps 8;

QY 1 MDKYDVIRKAGGAFGKAYLAGKSDSKHCVIKENFEKMPIOEKEASKKEVILLENKXKH 60

DB 1 MEKYERIRVVGGAFGVHLCLRKADQKLVIIKQIPVEQMTKEBQAQNECQVLKLNH 60

QY 61 PNIVAFNFGQENGRLFIVMEYCDGDLMKRINRQGVLFSDQILGFVQISGLKXHH 120

DB 61 PNIVIEYENFLEDKALMTAMEYAPGGLTAAEFIQKRCNSLLEETILHFFVQILLALHHV 120

QY 121 DRKILHRDIKAONIPLSKNGMVAKLDFGIARVLNNSMELARTCIGTPYVLSPICONKP 180

DB 121 THLLHRLDKTONILLDKRWVVKIGDFGISKIL-SKSKAYTVVGVTCYISPLCEGKP 179

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 240

DB 180 YNNKSDIWSLGCVLVELASLKRPEAANLPALVKIMSGTFAPISDRYSPELQVLVSL 239

QY 241 QVSPDRPINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASRHAGVQK-- 298

DB 240 SLEPAQRPLSHMAQPLCIRALLNLHTD-----VGSVMRRAEKSVAASN 285

QY 299 --CKYQVRFG--KCPPRSISVPIK-----RNALLHNRNEWPPAG-AQKA 340

DB 286 TGSRTTSVRCRGPGRVPAIPPELSSVYAWGGGLGTPLPLMLNTEVWQVAAAGRTQA 345

QY 341 --RGIKMI--BRPKIAA 353

DB 345 GVTRSGRLLEWAPLGA 363

RESULT 6

US-09-167-206-2

Sequence 2, Application US/09167206A

Patent No. 6476193

GENERAL INFORMATION:

APPLICANT: Nardabalan, Krishnan

APPLICANT: Schuiz, Vincent P.

APPLICANT: Yang, MeiJa

TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES

FILE REFERENCE: 15966-521 NIK1 protein complexes

CURRENT APPLICATION NUMBER: US/09/167,206A

CURRENT FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 445

TYPE: PRT

ORGANISM: Homo sapiens

US-09-167-206-2

Query Match 22.8%; Score 816.5; DB 3; Length 345;

Best Local Similarity 44.9%; Pred. No. 18-56;

Matches 173; Conservative 55; Mismatches 80; Indels 77; Gaps 6;

QY 1 MDKYDVIRKAGGAFGKAYLAGKSDSKHCVIKENFEKMPIOEKEASKKEVILLENKXKH 60

DB 1 MEKYVRLQIGEGSGKALVKSSTEDGRQYVIKENISEMSKEREESREAVLANVXKH 60

QY 61 PNIVAFNFGQENGRLFIVMEYCDGDLMKRINRQGVLFSDQILGFVQISGLKXHH 120

DB 61 PNIVQYRESF-----EGILDWFVQICLALKXHV 88

QY 121 DRKILHRDIKAONIPLSKNGMVAKLDFGIARVLNNSMELARTCIGTPYVLSPICONKP 180

DB 89 DRKILHRDIKSONIFLTQGTGV-QLGDFGIARVLNSTVELARTCIGTPYVLSPICONKP 147

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 240

DB 148 YNNKSDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 207

QY 241 QVSPDRPINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGA---PASRAG--- 293

DB 208 KRNPRDRPNSVLSLEKGFATAKIEFLSPQLAEFCLTKSPKSGQIPAKRPASQNS 267

QY 294 -----KVQCKIKQVRFGCKCPPRSISVPIKNAI 325

DB 268 ISVMPAQKITPAKYGIFLAYKKGDKLHKKPLQKH-QAHQTPEKRYNTGEERRKI 326

QY 326 LHRNEWPPAGAKARSIKMIERPCK 350

DB 327 SEB-----AARKRLRLEFIEKDK 343

RESULT 5

US-09-992-481-2

Sequence 2, Application US/0992481

APPLICANT: Mathur, Brian

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. 6593125e1 Human Kinases and Polynucleotides

TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0266-USA

CURRENT APPLICATION NUMBER: US/09/992,481

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: US 60/252,011

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 692

TYPE: PRT

ORGANISM: homo sapiens

US-09-992-481-2

Query Match 17.5%; Score 634; DB 4; Length 692;

Best Local Similarity 38.9%; Pred. No. 7.6e-42;

Matches 147; Conservative 63; Mismatches 128; Indels 40; Gaps 8;

QY 1 MDKYDVIRKAGGAFGKAYLAGKSDSKHCVIKENFEKMPIOEKEASKKEVILLENKXKH 60

DB 1 MEKYERIRVVGGAFGVHLCLRKADQKLVIIKQIPVEQMTKEBQAQNECQVLKLNH 60

QY 61 PNIVAFNFGQENGRLFIVMEYCDGDLMKRINRQGVLFSDQILGFVQISGLKXHH 120

DB 61 PNIVIEYENFLEDKALMTAMEYAPGGLTAAEFIQKRCNSLLEETILHFFVQILLALHHV 120

QY 121 DRKILHRDIKAONIPLSKNGMVAKLDFGIARVLNNSMELARTCIGTPYVLSPICONKP 180

DB 121 THLLHRLDKTONILLDKRWVVKIGDFGISKIL-SKSKAYTVVGVTCYISPLCEGKP 179

QY 181 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQOLVLIKQAHFAPISPGFSRELHSLISQLF 240

DB 180 YNNKSDIWSLGCVLVELASLKRPEAANLPALVKIMSGTFAPISDRYSPELQVLVSL 239

QY 241 QVSPDRPINSILKRPFLNLI PKYLTPEVIOEFSHMLICRAGAPASRHAGVQK-- 298

DB 240 SLEPAQRPLSHMAQPLCIRALLNLHTD-----VGSVMRRAEKSVAASN 285

QY 299 --CKYQVRFG--KCPPRSISVPIK-----RNALLHNRNEWPPAG-AQKA 340

DB 286 TGSRTTSVRCRGPGRVPAIPPELSSVYAWGGGLGTPLPLMLNTEVWQVAAAGRTQA 345

QY 341 --RGIKMI--BRPKIAA 353

DB 345 GVTRSGRLLEWAPLGA 363

RESULT 6

US-09-167-206-2

Sequence 2, Application US/09167206A

Patent No. 6476193

GENERAL INFORMATION

```

QY      2  DKYDVWIKAGOGAFGKAYLAKGKSDSKXCHVKEINFEMKPIQBEKASKEVILLKMKHP 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      6  EDYEVLYTIGTSYGRCKIRKSDGKILYWKELDYGSMTEABQKMLVSEVNLRELKHP 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     62  NIVAFNFNSF--QENGRLPVMVEYCGDGLMKRI--NRQGVLFVSEDOILGMFWVOISLGL 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     66  NIVRYDRIIDRTNTLLYVMEYCEGGDLASVITKTKEROYL--DEBFVLRVMTQLTAL 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    117  KTHDRK-----ILHRTIKAONIFLSKXGMAKLGDFGIARVLNNSMELATCIGTPYVL 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    125  KECHRRSDGHTVLHRDLKPAVFLDQKQV--KLGDFLGARIINHDTSPAKTFFVGTPTYM 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    172  SPEI CONKPYNNKTDIWSLGVLYELCTLKHPPFEGNNLQOLVKI CQAHFAPISPGFSRE 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    184  SPEQNNRMSYNEKSDIWSLGLLYELCALMPPTAFSQKELAGKIREGFRRI PYRYSDE 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    232  LHSLSIQLFQVSPDRPDSINSILKRPFLNLI PKYLTPEVIQEFSHMLICRA---GAP- 287
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    244  LNEIITRMLNLKQVHRPSVESILENPJADL-----VADEQRNLERRGOLGSPPE 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    288  ASRHAGKVQKQIKVRFQKCPRSRISVIPKRNAILHRNWRPAPGAQK-----339
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    295  KSQDSSPVLSELKKEIQI-----ERERALKARERLEQEQELCVRERLA 341
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    340  -----ARSIKWIERPIAAVCGHYDYVAQLDMLRRRAHKSHYHPIQENTGVED 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    342  EDKLARAENLKNVSLKERFLSLANPELLNPSSVIKKVH-----FSGESKENI---- 394
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    390  YQGETRHGFPSPQWPAEYLQKFBAAQ-----YKLKVEKQOLGR 428
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    395  MRSENSEBQLTSSKSKCDLKRHLHAAQLRAQALSDIEKNYQKSRQILGWR 445
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 7

US-08-870-529-2

```

: Sequence 2, Application US/08870529
: Patent No. 6080557
: GENERAL INFORMATION:
: APPLICANT: Sims, John E.
: APPLICANT: Virca, G. Duke
: APPLICANT: Bird, Timothy A.
: APPLICANT: Anderson, Dirk M.
: TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED AND BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/870,529
: FILING DATE: 06-JUN-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mcmasters, David D.
: REGISTRATION NUMBER: 33,963
: REFERENCE/DOCKET NUMBER: 480052.418
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 622-6031
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 979 amino acids
: TYPE: amino acid

```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-870-529-2

Query Match          14.8%; Score 535.5; DB 3; Length 979;
Best Local Similarity 40.7%; Pred. NO. 7.8e-34;
Matches 105; Conservative 55; Mismatches 95; Indels 3; Gaps 2;

QY      4  YDVIKAIGGAGKAYLAKGSKSHCVIKKINFERKMPIQKEAKSKEVILLKMKHPNI 63
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      52  YPIRVLGRGAGEATLYRTEDDLSLVVWKEVDLTPLSEKERRDALNEIVILALQHDNI 111

QY      64  VAFNFSQENGRLFTVMEYCDGGLMKRINRQGVLFSEDDILGWVFQISLGLKHTHDKR 123
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      112 IAYVNHFMONTLLILEYCNCGNLVKDKLRQDKLFEEMVWYLFQIVSAVSCIHKAG 171

QY      124 ILHRDITKAONIPLSKNGMVAKLGDFGIARVLNNSMELATCTGTPYVLSPELCONKPYNN 183
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      172 ILHRDITKUNIELTKANLI-KLGDYGLAKLNSYMSMATLVGTPTPYMGPELCQGVKNF 230

QY      184 KTDIWSLGLCVLYELCTLKHFFEGNNLQQVLKTCQAHFA--PISPGFSELHSLISQLFQ 241
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      231 KSDIWAAGCVIFELLTLKETFDATPNLNCVKLVQIGIRAMEVDSSQYSELQVHSCLD 290

QY      242 VSRDRSPSINSILKRPFLL 259
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      291 QDPEQRPTADELLDRPLL 308
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

## RESULT 8

```

US-09-544-794-2
; Sequence 2, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-794-2

```

[illegible]

Qy 242 VSPDRPSPINSILKRPFL 259  
Db 291 QDEQRPTADELLDRPLL 308

## RESULT 9

US-09-457-040B-18  
; Sequence 18, Application US/09457040B  
; Patent No. 6387641  
; GENERAL INFORMATION:  
; APPLICANT: Vertex Pharmaceuticals Incorporated  
; APPLICANT: Bellon, Steve  
; TITLE OF INVENTION: Crystallized P38 Complexes  
; FILE REFERENCE: VPI/98-14  
; CURRENT APPLICATION NUMBER: US/09/457,040B  
; CURRENT FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 18  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: EMENI - Aspergillus nidulans  
US-09-457-040B-18

Query Match 14.3%; Score 517.5; DB 4; Length 699;  
Best Local Similarity 25.8%; Pred. No. 1.3e-32;  
Matches 185; Conservative 104; Mismatches 244; Indels 183; Gaps 28;  
Qy 2 DKYDVIKAGCGAFKAYLAKGKSDSKHCVKEINFEKMPQOEKASKEVILLEKMKHP 61  
Db 9 DYEVEKIGCGSGFIIKVKKSGDFILCKEINIKMSYKERQLTAEFNILSSLRHP 68  
Qy 62 NIVAFPN--SPQNGRLFTVMEYCDGDL-----MKRINRQGVLFSEDOILGFV--Q 111  
Db 69 NIVAYHREHLKASQDLVLYMEYCGGDL--SVMIKLNKRTNK-----YAEEDFV-WRILSQ 122  
Qy 112 ISLGLKHIIH-----DKILHROITKQNIPLSKNGMYAK 144  
Db 123 LVIALYRCHYGTDPRAEVGSLNGLGPAKPSGLKGAQMTILHRDUPENIFLGSNTV-K 181  
Qy 145 LGDFGIARVNNMSELTCTGTPYLSPEIQNPKYNNKTDIWSLGVLYELCTLKHFF 204  
Db 182 LGDFGLSKLM-HSHDFASTYVGTTFVMSPEICAAEKYTLRSDIWAVGCMYELCQREPPF 240  
Qy 205 EGNINQOLVKIQAHFAPISGFBREHLISLQSFQVSPDRPSPINSILKRPFLNLP 264  
Db 241 NARTHQLVQKIREGKAPLPDYSSELKNVIAASCLRVNPDHPTATLINTPVI----- 295  
Qy 265 KYLTPEVIEBPSHMLICRAGAPAGRHAGKVQK--CKIQKVFQKCPPRSISVPTKR 322  
Db 296 RLMREVELNLSR--AAKREKREATWQAKDVEQAFKLEKEKQ-----IRSELENSLR 349  
Qy 323 NAILHRNEWRPAGAKARSIKVIERPXIAVCGHYDYVYAQLDMLRRRAHKPSVHPPIQ 382  
Db 350 -----EMEVARLEIDRQV-----NELDKLRKFECEQVDRVAQ 384  
Qy 383 ENTGVEDYQETHGSPSPQAEVYLQRFKFAQQKLVKQGLGRPSAEPNTYNOEL 442  
Db 385 E-----VEKQ-----RRNATREDASL 401  
Qy 443 RSGBEPRFQELPRKNMEQYWKQLEIRQQYHNDMKEIRKMGREPEENSKISHKT 502  
Db 402 RSGSHSSQSSNSDPSSTDISQLS--LESPTNKAALKPKESRTPTTRSK----- 454  
Qy 503 YLVKSNLPVHODAGEGAPVODIEKDLKQPLQNTKSKQPEQYKAKKGKVEINLDK 562  
Db 455 -TVVSPMDIQM---AEPSPIASLSLSPKTSATYSGKNIFABGERKR-PKFEPTL--- 507  
Qy 563 CISDENILOEBEAMDIPNET--LTEDGMKFEYECVKEHGDYTDKAFELKLCPEAGFST 620  
Db 508 AYSDO-----EDTPELPSPTRKVPKPPKAPSRRLLRQN---TVALQKL-----ST 553

Qy 621 QTVAAGNRRQWDGGAQTILLQMMVADITSTCTGPDGSESVLSVRQEGTKTDPY 676  
Db 554 QPIFFAN-----PSRLPQMSA-----PDV-----RESKSRSPH 582

## RESULT 10

US-09-221-235-2  
; Sequence 2, Application US/09221235  
; Patent No. 6043040  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/221,235  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; EARLIER FILING DATE:  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-221-235-2

Query Match 12.8%; Score 462.5; DB 3; Length 302;  
Best Local Similarity 37.1%; Pred. No. 9.3e-29;  
Matches 95; Conservative 54; Mismatches 100; Indels 7; Gaps 5;  
Qy 4 YDVIKAGCGAFKAYLAKGKSDSKHCVKEINFEKMPQOEKASKEVILLEKMKHPN 62  
Db 34 FRIEKKIGRQFSEVTRACLLDGVPAVKKVOIFLMDAKARADCIKEIDLKQLNHPN 93  
Qy 63 IVAFFNSFQNGRLFTVMEYCDGDLMKRIN--RQGVLFSEDOILGFVQISLGLKHIIH 120  
Db 94 VIKYVASFIEDNEINLIVLELADAGDLSRMTKHKQKRLIPERTVWKYFVQLCSALEHMH 153  
Qy 121 DRKILHRDITKQNIPLSKNGMYAKLGDGFTARVNNMSELTCTGTPYLSPEIQNKP 180  
Db 154 SRVMMHRDIAPNVITATGVV-KUGDLGRFSSKTTAAHSLVGTPTMSPERTHENG 212  
Qy 181 YNNKTDIWSLGVLYELCTLKHFFEGN--NLQOLVLKIQAHFAPIT-SPOFSPRELHSLIS 237  
Db 213 YNFKSDIWSLGLLYEMAALQSPFYGDKNLYSLCKKIEQCDVPPLPSDHYSELQVLN 272  
Qy 238 QLFQVSPDRPSPINSI 253  
Db 273 MCINPDPEKRPDVTYV 288

## RESULT 11

US-09-221-928-2  
; Sequence 2, Application US/09221928  
; Patent No. 6121030  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/221,928  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; EARLIER FILING DATE:  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-221-928-2

Query Match 12.8%; Score 462.5; DB 3; Length 302;  
Best Local Similarity 37.1%; Pred. No. 9.3e-29;  
Matches 95; Conservative 54; Mismatches 100; Indels 7; Gaps 5;



Search completed: October 8, 2004, 17:09:58  
Job time : 24 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2004, 17:01:35 ; Search time 15 Seconds  
(without alignments)  
2370.928 Million cell updates/sec

Title: US-09-940-921B-2  
Perfect score: 3616  
Sequence: 1 MDKVDVKAIGCGAGKAYL.....SVSRQEGTKDYPSPVILM 683

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1106.5	30.6	774	1 NEK1 MOUSE	P51954 mus musculu
2	1063.5	29.4	1258	1 NEK1 HUMAN	Q96py6 homo sapien
3	808.5	22.4	511	1 NEK3 MOUSE	Q9r0a5 mus musculu
4	808	22.3	506	1 NEK3 HUMAN	P51956 homo sapien
5	665.5	18.4	792	1 NEK4 MOUSE	Q921j2 mus musculu
6	660	18.3	841	1 NEK4 HUMAN	P51957 homo sapien
7	634	17.5	592	1 NEK8 HUMAN	Q858g6 homo sapien
8	633	17.5	598	1 NEK8 MOUSE	Q921z4 mus musculu
9	623	17.2	697	1 NEK8 BRAVE	Q90xc2 brachydanio
10	539.5	14.9	445	1 NEK2 HUMAN	P51955 homo sapien
11	535.5	14.8	979	1 NEK9 HUMAN	Q8td19 homo sapien
12	532.5	14.7	443	1 NEK2 MOUSE	O35942 mus musculu
13	532.5	14.7	984	1 NEK9 MOUSE	Q8k1r7 mus musculu
14	524.5	14.5	944	1 NEK9 XENLA	Q7z2c8 xenopus lae
15	521.5	14.4	431	1 NRKA TRYBB	Q08942 trypanosoma
16	517.5	14.3	699	1 NIMA EMENI	P11837 emericella
17	511	14.1	722	1 FIN1 SCHPO	O13839 schizosacch
18	490	13.6	431	1 NRK3 TRYBB	Q03428 trypanosoma
19	472.5	13.1	313	1 NEK6 RAT	P59895 rattus norv
20	471.5	13.0	313	1 NEK6 HUMAN	Q9hcn9 homo sapien
21	469.5	13.0	213	1 NEK6 MOUSE	Q9s870 mus musculu
22	464.5	12.8	779	1 NIM1 NEUCR	P48479 neurospora
23	462.5	12.8	302	1 NEK7 HUMAN	Q8tdx7 homo sapien
24	458.5	12.7	302	1 NEK7 MOUSE	Q9es74 mus musculu
25	423	11.7	435	1 KIN3 YEAST	P22209 saccharomyc
26	405	11.2	576	1 POLO DROME	P52304 drosophila
27	402.5	11.1	1576	1 YLK3 CAEEL	P41951 caenorhabdi
28	395	10.9	1360	1 TNK1 HUMAN	Q9uke5 homo sapien
29	392.5	10.9	966	1 STKA MOUSE	O55098 mus musculu
30	392	10.8	1142	1 GIN4 YEAST	Q12263 saccharomyc
31	391	10.8	658	1 PAK1 SCHPO	P50527 schizosacch
32	389	10.8	968	1 STKA HUMAN	O94804 homo sapien
33	388	10.7	705	1 CDC5 YEAST	P32562 saccharomyc

34	388	10.7	1050	1 ULK1 HUMAN	O75385 homo sapien
35	387.5	10.7	1051	1 ULK1 MOUSE	O70405 mus musculu
36	382.5	10.6	982	1 SULU CAEEL	P46549 caenorhabdi
37	379	10.5	682	1 SNK MOUSE	P53351 mus musculu
38	379	10.5	752	1 K6A2 CHICK	P18652 gallus galli
39	379	10.5	856	1 UN51 CAEEL	Q23023 caenorhabdi
40	378	10.5	490	1 SPS1 YEAST	P08458 saccharomyc
41	378	10.5	682	1 SNK RAT	Q9r012 rattus norv
42	378	10.5	685	1 SNK HUMAN	Q9nyy3 homo sapien
43	378	10.5	1308	1 M4K6 MOUSE	Q9jw52 mus musculu
44	378	10.5	1332	1 M4K6 HUMAN	Q8n4c8 homo sapien
45	376	10.4	733	1 K6A2 HUMAN	Q15349 homo sapien

ALIGNMENTS

RESULT 1

ID	NEK1 MOUSE	STANDARD;	PRT;	774 AA.
AC	P51954;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Serine/threonine-protein kinase Nek1 (EC 2.7.1.37) (Nima-related protein kinase 1).			
DE	protein kinase 1).			
GN	NEK1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=93010942; PubMed=1382974;			
RA	Letwin K., Mizzen L., Motro B., Ben-David Y., Bernstein A.,			
RA	Pawson T.;			
RT	"A mammalian dual specificity protein kinase, Nek1, is related to the NIMA cell cycle regulator and highly expressed in meiotic germ cells".			
RL	EMBO J. 11:3521-3531 (1992).			
CC	-!- FUNCTION: PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF MEIOSIS.			
CC	-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	-!- SUBCELLULAR LOCATION: Nuclear (Probable).			
CC	-!- TISSUE SPECIFICITY: PREDOMINANTLY IN TESTES (GERM CELLS AND SERTOLI CELLS). LOWER LEVELS IN OVARY (OVOCYTES AND GRANULOSA CELLS), THYMUS, AND LUNG.			
CC	-!- DEVELOPMENTAL STAGE: IN FEMALE, EXPRESSED AS FOLLICLES ENTER THE SECONDARY STAGE UNTIL OVULATION OCCURS. IN THE MALE REPRODUCTIVE SYSTEM, THE EXPRESSION IS LIMITED TO SPERMATOCYTES AND SPERMATIDG.			
CC	-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA subfamily.			

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CC	EMBL; S45828; AAB23529.1; -.
CC	PIR; S25284; S25284.
CC	HSSP; Q63450; 1A06.
CC	MGD; MGI:97303; Nek1.
CC	InterPro; IPR000719; Prot_kinase.
CC	InterPro; IPR008271; Ser_Thr_pkin_AS.
CC	InterPro; IPR002290; Ser_Thr_pkinase.
CC	InterPro; IPR001245; Tyr_pkinase.
CC	Pfam; PF00069; pkinase; 1.
CC	PRINTS; PR00109; TVRKINASE.





DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;  
KW Nuclear protein; Phosphorylation; Cell cycle; Cell division;  
KW Tyrosine-protein kinase; Alternative splicing.  
FT DOMAIN 4 258 PROTEIN\_KINASE.  
FT NP\_BIND 10 18 ATP (BY SIMILARITY).  
FT BINDING 33 33 ATP (BY SIMILARITY).  
FT ACT\_SITE 128 128 BY SIMILARITY.  
FT MOD\_RES 162 162 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT VARSPLIC 478 521 Missing (in isoform 2).  
FT FTIC=VSP 004870.  
FT CONFLICT 1232 1232 G -> E (IN REF. 2).  
SQ SEQUENCE 1258 AA; 142828 MW; 339C4BFA56612530 CRC64;  
Query Match 29.4%; Score 1063.5; DB 1; Length 1258;  
Best Local Similarity 33.4%; Pred. No. 8.7e-50;  
Matches 279; Conservative 122; Mismatches 232; Indels 203; Gaps 23;  
QY 1 MDKVDVIAIGAGFGKAVLAGKSDSKHCIVKEINFEKMPICQEAASKVILEKMKH 60  
DB 1 MEKYVRLQKIGSGFGKAILVKSTEDGQYVKEINISMSKEREERREAVLANWKH 60  
QY 61 PNIVAFNFSQNGRLFIWMEYCDGDLMKRINRGVLFSEDIQLGFVQISLGLKH 120  
DB 61 PNIVQVRESFEENGLYIMDYCEGDLFKRINAGKGVLFQEDQLDFVQICLAKH 120  
QY 121 DRKILHRIKADNIFLSKNGMTAKLGDGICARVLANSMELARTCIGTPYLSPEIC 180  
DB 121 DRKILHRIKADNIFLTKDGTV-QUGDFGIARVLANSTVELARTCIGTPYLSPEIC 179  
QY 181 YNNKTDIWSLGVLYELCTLKHFFEGNNLQQLVLCIQAHFAPISGFSRELHSLIS 240  
DB 180 YNNKSDIWSLGVLYELCTLKHFAEAGSMKNVLXIISGFPVPSLHYSYDLRLSVLS 239  
QY 241 QVSPDRPSINSILKRPFLNLIPIKLTPEVIOEFSHMLICRAGA---PSRHAG--- 293  
DB 240 KENPRDRPSVNSILEKGTAKIEKFLSPQLAEFCUKTFSKGSQIPAKRPSAGQNS 299  
QY 294 -----KVQCKIKQVRFQCKPPRSRISVPTKRWAI 325  
DB 300 ISVMPAQKITPAKXVGIPLAYKKYGDKLHEKPKLQXHK-QAHQTPKRVNTGEERKI 358  
QY 326 -----LHRNE-----WRPPAGAOKA 340  
DB 359 SBEAARKRLTEFEKEKKQKQDIISLMKAEQKROEKERLERINRAREQGNVLISAGGS 418  
QY 341 RSIKM-----IEPKIAAVCGHYDYIAQLD-MLRRRAHK-----PSYH 378  
DB 419 GEVKAPFLGGGTIAPSSFSRSGQYEHVHAIFDQMQQRAEDNEAKWKREYGRGLPERG 478  
QY 379 PIPQENTGVEDYGOETRH-----GFPSPQMPABY 407  
DB 479 ILPGVRPGF-PYGAAGHHFPDADDIRKTLKELKAVSQANRQKQLAVERAKQVEEF 537  
QY 408 LQKFEAQYKLVKVE-----KQLGRPSAPENYNORQELRS--NGEPRQELPF 456  
DB 538 LQKFEAQYKLVKVE-----KQLGRPSAPENYNORQELRS--NGEPRQELPF 456  
QY 457 RKNEMKEQYVWKOLEIRQOYHND---MKEIRKMGREPEENSKISHTKYLKKS----- 508  
DB 592 QEGSEADMRKIESLKAHANARAVALKEQLERKKEAYEREKKVWBEHLVAKGVKSSD 651  
QY 509 -NLPHQDASEGAPVQ-----DIEKOLKQM-----RLQNTKESKNPEOK-----YKAKG 553  
DB 652 VSPPLQGHETGGSPSQQRVSVISVTSALKVEGVDSLSLTDRTETSEEMQKTNNAISSRE 711  
QY 554 VKFEINLDCISDENTLQEEAMDIENETLTTFDGMKFKFEYECVKEHGDYTDK-----APE 609  
DB 712 ILRLN-----ENLKAQEDKGNLSDTTEINVHDEKHEKEKSVSSDRKKWEAGG 764  
QY 610 KLHCP-----EAGFSTQTVAAVGN-----RRQWDGAPOTLLQMMVAADI 649

DB 765 QLVIPDELTLDTSFSTTERTHTVGEVILKPNQSPRAWKSKPTDVLKILGEAL 820  
RESULT 3  
NEK3 MOUSE  
ID NEK3 MOUSE STANDARD; PRT; 511 AA.  
AC Q9ROA5; Q9ZOX9.  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Serine/threonine-protein kinase Nek3 (EC 2.7.1.37) (Nima-related protein kinase 3).  
GN NEK3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99240743; PubMed=10224116;  
RA Tanaka K., Nigg E.A.;  
RT "Cloning and characterization of the murine Nek3 protein kinase, a novel member of the NIMA family of putative cell cycle regulators.";  
RL J. Biol. Chem. 274:13491-13497(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=10393247;  
RA Chen A., Yanai A., Arama B., Kilfin G., Motro B.;  
RT "NIMA-related kinases: isolation and characterization of murine nek3 and nek4 cDNAs, and chromosomal localization of nek1, nek2 and nek3.";  
RL Gene 234:127-137(1999).  
CC CC  
CC -!- FUNCTION: Kinase that may play a role in mitotic regulation.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA subfamily.  
CC  
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CC  
CC EMBL; AF093416; AAD20986.1; -  
CC EMBL; AF099066; AAD16286.1; -  
CC HSP; O63450; 1A06.  
CC MGD; MGI:1344371; Nek3.  
CC InterPro; IPR000719; Prot\_kinase.  
CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
CC InterPro; IPR002290; Ser\_thr\_pkinase.  
CC InterPro; IPR001245; Tyr\_pkinase.  
CC Pfam; PF00069; pkinase; 1.  
CC PRINTS; PR00109; TYRKINASE.  
CC ProDom; PD000001; Prot\_kinase; 1.  
CC SMART; SM00220; S\_TKc\_1.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;  
KW Nuclear protein; Phosphorylation; Cell cycle; Cell division.  
FT DOMAIN 4 255 PROTEIN\_KINASE.  
FT NP\_BIND 10 18 ATP (BY SIMILARITY).  
FT BINDING 33 33 ATP (BY SIMILARITY).  
FT ACT\_SITE 125 125 BY SIMILARITY.  
FT MOD\_RES 159 159 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CONFLICT 239 239 N -> K (IN REF. 2).  
FT CONFLICT 342 343 MISSING (IN REF. 2).  
SQ SEQUENCE 511 AA; 57222 MW; DB6D6C0533C7302F CRC64;  
Query Match 22.4%; Score 808.5; DB 1; Length 511;  
Best Local Similarity 33.1%; Pred. No. 1.4e-36;  
Matches 202; Conservative 99; Mismatches 193; Indels 117; Gaps 16;

QY 1 MDKYDVIAKAGGATGKAVLAKGSDSKHCYVKEINFEKMPQIOEKASKEVILEKMKH 60  
 Db 1 MONTYVLRVIGGSGFRALVUQESNQTFAKKEIRLLK---SDTQTSRKEAVLLAKMKH 57  
 QY 61 PNIVAFPSFQNGRLFIWMEYCDGDLMKRINRQGVLFSDQILGWFOVSIQGLKHII 120  
 Db 58 PNIVAFKSEFEAGVLYIWMEYCDGDLMKRQKQGNLPEDTILNFIQICLVNHHI 117  
 QY 121 DRKILHRDITKAOINIFLSKMGVAKLGDGFIARVLNNSMELARTCTGTPYISPEICQKP 180  
 Db 118 KRVVLHRDITKXNVFLTHNGKV-KLGDGFSARLLSSPMFACTVYGTPTYPYPPPIWENLP 176  
 QY 181 YNNKTDIWSLGVLYELCTLKHPPFGNNLQOLVLIKCOAHFAPISPGFSRELHSLISOLF 240  
 Db 177 YNNKSDIWSLGLLYELCALXHPFOANSWKNLILKCOGPHPLPALYCKLQGLVKOML 236  
 QY 241 QVSPDRPINSILKRPFLNLIPIKYLTPDEVTOEFESHMLICRAGAPASRHAGKVQCK 300  
 Db 237 KRNPSHRPSATLLCRGSLAPLVKLPQITRE-----YGEQILDEIK 280  
 QY 301 IQKVRFOGKCPPRSIRISVPIKRNAILHRNRPAGACAKARSIKMIERPKIAAVCGHYDY 360  
 Db 281 ISTPKMKK-----QDSNRVGRALGEANSAAMQEEER-GRKCSHTE- 320  
 QY 361 YYAQLDMLERRAHKPSYHPIPOENTGVBDYGOETHGPPSQWPAEYLQKFEAQVYK 420  
 Db 321 -----LESTGTTAGNALGRAAGNPESGNRQEHGSHTS--PASPHRPRWERH----- 366  
 QY 421 VEKQLGLRPSAPYVNRQELRSNGEERPEQLPFRKNMEQEVYKWLQLEIEIQOYHND 480  
 Db 367 -----GPSSNVLEAKASILTSS-----FTAEDDRGGSVIKYEENARQWRE 409  
 QY 481 MKEIRKMGREPEENS KISHKTYLVKXGNL-----PVHQDASGEAPVQDIEXDLQMR 534  
 Db 410 PPEALLSLMKDADLSQ--AFQTYTYRFGAEGFLKGLPSEDTAS-----DSVDGDLDSVM 462  
 QY 535 LQNTKESKNPEQYKAKGVKFEINLDRKICSDENILQEEBAMDIPNETLTEDGKMKFEY 594  
 Db 463 L-----DPE-----RFEPLRDE--SDTOFEDNPNPDWSE----- 491  
 QY 595 ECVKHEGHDYTD 605  
 Db 492 --LKHVGYGD 500  
 RESULT 4  
 ID NEK3 HUMAN STANDARD; PRT; 506 AA.  
 AC P51956; Q8WUN5;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Serine/threonine-protein kinase Nek3 (EC 2.7.1.37) (Nima-related  
 protein kinase 3) (HSPK 36).  
 GN NEK3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE OF 48-506 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94366699; PubMed=7522034;  
 RA Schults S.J., Fry A.M., Suetterlin C., Ried T., Nigg E.A.;  
 RT "Cell cycle-dependent expression of Nek2, a novel human protein  
 kinase related to the NIMA mitotic regulator of Aspergillus  
 nidulans.";  
 RL Cell Growth Differ. 5:625-635 (1994).  
 RN [3]  
 RP SEQUENCE OF 76-189 FROM N.A.  
 RX MEDLINE=94100173; PubMed=8274451;  
 RA Schults S.J., Nigg E.A.;  
 RT "Identification of 21 novel human protein kinases, including 3  
 members of a family related to the cell cycle regulator nima of  
 Aspergillus nidulans.";  
 RL Cell Growth Differ. 4:821-830 (1993).  
 CC -!- FUNCTION: Kinase that may play a role in mitotic regulation.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA  
 subfamily.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; BC019916; AAH19916.2; -;  
 DR EMBL; Z29067; CA82310.1; -;  
 DR EMBL; Z25434; CA80921.1; -;  
 DR FIR; I38224; I38224.  
 DR HSP; Q00534; IBI7.  
 DR Genew; HGNC:7746; NEK3.  
 DR GK; P51956; -;  
 DR MIM; 604044; -;  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR GO; GO:0005824; F:ATP binding; NAS.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 DR GO; GO:0007049; P:cell cycle; NAS.  
 DR GO; GO:0007067; P:mitosis; NAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser Thr pkin AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE-ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;  
 FT Nuclear protein; Phosphorylation; Cell cycle; Cell division.  
 FT DOMAIN 4 257 PROTEIN KINASE.  
 FT NP BIND 10 18 ATP (BY SIMILARITY).  
 FT BINDING 33 33 ATP (BY SIMILARITY).  
 FT ACT SITE 127 127 BY SIMILARITY.  
 FT MOD\_RES 161 161 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

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FT CONFLICT 54 54 L -> S (IN REF. 2).
FT CONFLICT 77 78 IV -> LY (IN REF. 3).
FT CONFLICT 187 189 SIG -> RSV (IN REF. 3).
SQ SEQUENCE 506 AA; 57704 MW; 4437EB441A4777 CRC64;

Query Match
Best Local Similarity 34.1%; Pred. No. 1.5e-36;
Matches 196; Conservative 97; Mismatches 180; Indels 102; Gaps 16;

QY 1 MDKYDVIKAGGAKGKAVLAKGSKDVKHCIVKEINFEKMPQIOEAKSKVEVILLKMKH 60
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 PNIVAFNSFQNGRLFIWVEYCDGDLMKRINRQGVLFSDQILGHFVQISLGLKHIH 120
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 60 PNIVAFKESFEAGHLIYVWECDDGLMKQIKQKGLFPEDMLNFWFTQWCLGVNHIH 119
QY 121 DKILHRDIKAQNIPLSKNGVAKLGDGFIARVLNNSMELATCTGTTPYVSPETCNKP 180
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 KRVLRHDIKSNVIFLTQNGKV-KLGDGFGARLNSPMFACTVYVGTTPYVPEIENLP 178
QY 181 YNNKTDIWSLGVLYELCTLKHPPFGNNLQQLVLTQAHFAPISPGFSRELHSLISOLF 240
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 YNNKSDIWSLGVLYELCTLKHPPFQANSWNILKVCQGCISPLSHYSYELQFLVKQMF 238
QY 241 QVSPDRPINSILKRPFLNIPKYLTPDEVQEEFSLMILCRAGAPASRHAGKVYQCK 300
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 KNPGRPSATLLSGRIVARLVQKCLPPEITME-----YGEVLEBIK 282
QY 301 IQKVRPQGCPRPSRISVPIKENAILHRNEWPPAGAKARSIKMIERPAAVCGHYDY 360
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 283 NKNHTPRKTPNPSRIRIALGNEASTVQEEQDRKGS----- 319
QY 361 YYAQLDMLRRRAKPSYHP IPOENTGVEDYQGETRHGPPSPS-----QWPAEYLQKFEAQ 416
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 417 YKLKVEKQLGLPSPAEPNPNQRLSN--GEPR-FQELPFRKVENKQBYWQLEBI 473
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 364 -----EKNV---PNTALTALNASILTSLTAEDDRGGSVIKSKNTTRKQ--W--LKET 411
QY 474 RQCYHNDMKEIRKMGREPEENSKI-SHTKTYLV-----KSNLPVHQDASEG-----E 520
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 412 PDLTLNLK-----NADLSLAFQTYTYRPGSEGLKGLPSETEASDSVDGHDH 461
QY 521 APVQD---IEKDLKQMLQNTKESKNPEQKYAKK 552
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 462 SVILDPERLEPGLDEEDTDFEEDDNPQWVSELKK 496

RESULT 5
NEK4_MOUSE
ID NEK4_MOUSE STANDARD; PRT; 792 AA.
AC Q921J2; O35673; Q9RLJ1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase Nek4 (EC 2.7.1.37) (NIMA-related protein kinase 4) (Serine/threonine protein kinase 2).
GN NEK4 OR STK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=20001940; PubMed=10529384;
RA Hayashi K., Igarashi H., Ogawa M., Sakaguchi N.;
RT "Activity and substrate specificity of the murine STK2
RT serine/threonine kinase that is structurally related to the mitotic
RT regulator protein NIMA of Aspergillus nidulans.";
RL Biochem. Biophys. Res. Commun. 264:449-456(1999).

[2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=9321807; PubMed=10393247;
Chen A., Yanai A., Arama E., Kilfin G., Motro B.;
"NIMA-related kinases: isolation and characterization of murine nek3,
and nek4 cDNAs, and chromosomal localization of nek1, nek2 and nek3.";
Gene 234:127-137(1999).
CC -!- FUNCTION: Seems to act exclusively upon threonine residues.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=mSTK2L;
CC IsoId=Q921J2-1; Sequence=Displayed;
CC Name=2; Synonyms=mSTK2S;
CC IsoId=Q921J2-2; Sequence=VSP_007001;
CC -!- TISSUE SPECIFICITY: Expressed ubiquitously among various organs
CC and is upregulated in the testis.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA
CC subfamily.
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EMBL; AJ223071; CAAL1072.1; -.
EMBL; Y05234; CAA70436.1; -.
EMBL; AF099067; AAD16287.1; -.
PIR; JC7122; JC7122.
DR HSSP; Q63450; 1A06.
MGD; MGI:1344404; Nek4.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR003271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferrase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
Nuclear protein; Phosphorylation; Alternative splicing.
DOMAIN 6 261
FT NP_BIND 12 20 ATP (BY SIMILARITY).
FT BINDING 35 35 ATP (BY SIMILARITY).
FT ACT_SITE 131 131 BY SIMILARITY.
FT MOD_RES 165 165 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPPLIC 456 503 Missing (in isoform 2).
FT FTId=VSP_007001.
FT CONFLICT 499 499 G -> R (IN REF. 2).
SQ SEQUENCE 792 AA; 88994 MW; CF9187311C807ALD CRC64;

Query Match
Best Local Similarity 25.3%; Pred. No. 1.1e-28;
Matches 189; Conservative 137; Mismatches 213; Indels 209; Gaps 23;

QY 4 YDVIKAGGAGKAVLAKGSKDVKHCIVKEINFEKMPQIOEAKSKVEVILLKMKHPNI 63
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 6 YCYNVVRGSGSYGEVILVKHRRDGKQYVIKMLNRNASSERRAARAEQALLQLKHPNI 65
QY 64 VAFNSFQ-ENGRFLFVMEYCDGDLMKRINRQGVLFSDQILGHFVQISLGLKHIHR 122
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 66 VTYKESMEGGDGLIYVWGCEGDLRYLKEQGLLPESQVVFVQIAMAQLYLHEK 125
QY 123 KILHRDIKAQNIPLSKNGVAKLGDGFIARVLNNSMELATCTGTTPYVSPETCNKPYN 182
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 126 HILHRDILKQNIPLSKNGVAKLGDGFIARVLNNSMELATCTGTTPYVSPETCNKPYN 184
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QY 389 DYQG-----ETHGSPSPS-----QW-----PAEYLQKRFQAQYKUK----- 420
Db 402 SISQVEEEMLODNTRSSAQPENLIPWMSDDIVTGEKNEPVKPLQPLIKEQKPKQSLALS 461
QY 421 -----PKLECSGTLAHNURLGSSDSPASASRVAGITGVCHHAQDVQVAGECIIKQGRHPDL 521
Db 462 PKLECSGTLAHNURLGSSDSPASASRVAGITGVCHHAQDVQVAGECIIKQGRHPDL 521
QY 430 -----SSAPNPNV-QRQELRSNGEPR-----FQELPFR-----KN 459
Db 522 QPHNSGSPSLSRQKRRQREQTREKQKQVRRLDFAFQESPPRFLPSHPHIVGKVDVTS 581
QY 460 ENKEOEYKQ-----LEIRQYHDMKE-----IRKMGREPEENSKISHKYLKYS 508
Db 582 TOKENAGRRVVTGVSSSRSSEMSSKDRPUSARERRRLKQSQEEMSSSPS-----VRKA 638
QY 509 NLPVHQDASGEAPYQD-----FEKDLKQML-----QNTRESKNPEQY 548
Db 639 SLSV---AGPGKQEQDPLPARRLSSDCSVTQERKQIHCLSEDLSSSTSTSDGSDGY 695
QY 549 KAKGVKPEINLDCISDENIL--OEEEMDIP--NETLTEDGKFKFEYECVKEHGDYT 604
Db 696 GSGKQCTEINALVOLMTQTLLKDSKESCEDVPVANPVSEFKLHRKYRDTLIL--HGKVA 753
QY 605 DXAFKELHCP 615
Db 754 EEA-EELHKE 763

RESULT 7
ID NEK8 HUMAN STANDARD; PRT; 692 AA.
AC Q86566; ORNDHL;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Serine/threonine-protein kinase Nek8 (EC 2.7.1.37) (NIMA-related
DE protein kinase 8) (NIMA-related kinase 12a).
GN NEK8 OR NEK12A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RA Huang C.Q., Wu S.L., Yu L.;
RP SEQUENCE FROM N.A.
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Nedwiedek M.N., Roig J., Lenz G., Avruch J.;
RP SEQUENCE FROM N.A.
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Ottenwelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,
RC Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for renal tubular integrity (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Predominantly cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA
CC subfamily.
CC -!- SIMILARITY: Contains 5 RCC1 repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY242354; AAC88243.1; -.
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DR EMBL; AY267371; AAF04006.1; -.
DR EMBL; AL833909; CAD38765.1; -.
DR Genew; HGNC:13387; NEK8.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000408; Reg_Chr_condens.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00415; RCC1; 1.
DR PRINTS; PR00633; RCNDNSATION.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00625; RCC1_1_FALSE_NEG.
DR PROSITE; PS00636; RCC1_2_FALSE_NEG.
DR PROSITE; PS00012; RCC1_3_5.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Repeat.
FT DOMAIN 4 258 PROTEIN_KINASE.
FT NP_BIND 10 18 ATP (BY SIMILARITY).
FT REPEAT 312 350 RCC1 1.
FT REPEAT 410 461 RCC1 2.
FT REPEAT 462 513 RCC1 3.
FT REPEAT 580 631 RCC1 4.
FT REPEAT 632 684 RCC1 5.
FT ACT_SITE 128 128 BY SIMILARITY.
FT BINDING 33 33 ATP (BY SIMILARITY).
FT MOD_RES 162 162 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 692 AA; 74806 MW; 9E03820DFB3D5CA1 CRC64;

Query Match 17.5%; Score 634; DB 1; Length 692;
Best Local Similarity 38.9%; Pred. No. 4.5e-27;
Matches 147; Conservative 63; Mismatches 128; Indels 40; Gaps 8;

QY 1 MDXYDVTKAIGOGAFGKAYLAKGKSDSKHCVKEINFERKMPQKEASKEVILLKMKH 60
Db 1 MEKIERIRVVRGAGFIVHLCURKADQKLVILKQIPVEQNTKEERAQNECOVLKLNH 60
QY 61 PNIVAFNSFQENGRLEFVMEYCDGGLMKRINRQGVLFSEDOILGWVQV-SLGLKH 120
Db 61 PNVEYVENFLEDKALMIAMEYAPGGTAEFIQKRCNSLEETILHFFVQILLALHHV 120
QY 121 DRKILHRDIKAOIFLSKNGVAKLGDGFIARVNNMSMELARTICITPTPYLSQNK 180
Db 121 THILHRDLKTQNLILDKHRMVVKIGDFGLSKIL-SSSKAYTVVGTPTCYISPELCE 179
QY 181 YNNKTDIWSLGCVLVEICTLKHFFEGNNILQQLVKICQAHFAPISPGFRELHSLIS 240
Db 180 YNQKSDIWLGCVLVEYELASLKRAFEANLPAVLKIMSGTFAFISDRYSPQLVLSLL 239
QY 241 QVSPRRPSPINSILKRPFLNLPKYLTPETVEQEEFESHMLICRAGAPASRHACKV 298
Db 240 SLEPACRPPLUSHIMAOPLCIRALLNLHTD-----VGSVRVRRRAEKSVAPSN 285
QY 299 --CKIQKVRQG--KCPPRSISVPITK-----RNAILHRNWRPDPAG-AQKA 340
Db 286 TGSRTTSVRCRGIPRGFVRPAIPPLSSVYVWGGLGTPLRLPMLNTEVVQVAGRTQ 345
QY 341 ---RSIKMI--ERPRTAA 353
Db 346 GVTRSGRLILWEAPPLGA 363

RESULT 8
NEK8 MOUSE STANDARD; PRT; 698 AA.
ID NEK8 MOUSE Q91ZRA; Q9D685;
AC Q91ZRA; Q9D685;
DT 10-OCT-2003 (Rel. 42, Created)
```

10-OCT-2003 (Rel. 42, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 Serine/threonine-protein kinase Nek8 (EC 2.7.1.37) (NIMA-related  
 protein kinase 8).  
 NEK8.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]\_TaxID=10090;  
 SEQUENCE FROM N.A. (ISOFORM 1), MUTAGENESIS OF LYS-33, AND VARIANT  
 ARKPKD VAL-448.  
 STRAIN=C57BL/6J; TISSUE=Skin;  
 MEDLINE=21085660; PubMed=11217851;  
 Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 Schriml L.M., Stauber F., Suzuki R., Tonita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,  
 Brownstein M.J., Bult C., Fleischer C., Fujita M., Kamiya M., Lee N.H.,  
 Gustingich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,  
 Hayashizaki Y.;  
 Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690(2001).  
 CC -!- FUNCTION: Required for renal tubular integrity. May regulate local  
 cytoskeletal structure in kidney tubule epithelial cells.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBCELLULAR LOCATION: Predominantly cytoplasmic.  
 CC -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Name=1;  
 IsoId=Q912R4-1; Sequence=Displayed;  
 Name=2;  
 IsoId=Q912R4-2; Sequence=VSP\_007959, VSP\_007960;  
 Note=due to intron retention. No experimental confirmation  
 available;  
 CC -!- TISSUE SPECIFICITY: Kidney, liver, and testis.  
 CC -!- DISEASE: Defects in NEK8 are the cause of autosomal recessive  
 juvenile polycystic kidney disease (ARPKD).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA  
 subfamily.  
 CC -!- SIMILARITY: Contains 5 RCC1 repeats.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF407579; AAL09675.1; -;  
 CC EMBL; AK014546; BAB29424.1; -;  
 CC MGD; MGI:1890646; Nek8.

DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR000408; Reg chr condens.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00415; RCC1; 3.  
 DR PRINTS; PR00633; RCCNDNGATION.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00625; RCC1\_1; FALSE\_NEG.  
 DR PROSITE; PS00626; RCC1\_2; FALSE\_NEG.  
 DR PROSITE; PS00112; RCC1\_3; 5.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Repeat; Alternative splicing; Disease mutation.  
 FT DOMAIN 4 258  
 FT NP\_BIND 10 18  
 FT REPEAT 416 467  
 FT REPEAT 468 519  
 FT REPEAT 520 585  
 FT REPEAT 586 637  
 FT REPEAT 638 690  
 FT ACT\_SITE 128 128  
 FT BINDING 33 33  
 FT MOD\_RES 162 162  
 FT VARSPPLIC 277 291  
 FT  
 FT VARSPLIC 292 698  
 FT VARIAT 448 448  
 FT MUTAGEN 33 33  
 FT  
 FT CONFLICT 15 15 F -> L (IN REF. 2).  
 FT CONFLICT 246 246 R -> G (IN REF. 2).  
 FT SEQUENCE 698 AA; 75264 MW; 686B29A8CF180E94 CRC64;  
 SQ  
 Query Match 17.5%; Score 633; DB 1; Length 698;  
 Best Local Similarity 38.0%; Pred. No. 5.2e-27;  
 Matches 147; Conservative 65; Mismatches 123; Indels 52; Gaps 9;  
 QY 1 MDKYDVIRKAGGAFKAYLAKGSDSKHCVTKEINFEMPIQKEASKVILEKMKH 60  
 Db 1 MEKYRIRVVGRGAFGI VHLCKRADQKLVILKQIPVEQMTKEERQAQNCQVLLNH 60  
 QY 61 PNIVAFNFSQNGRLFTVMEYCDGGLMKRINRQGVLFSEDDQILGWFOISLKH 120  
 Db 61 PNIVIEYENFLEDKALMIAMEYAPGGTLAEFTCKRCSLLEETILHFFVQILLALH 120  
 QY 121 DRKILHRDIKAQNI FLSKNGWAKLGDGFIARVLNNSMELATCTGTPYLSPEICNKP 180  
 Db 121 THLILHRDLKTONILLDKRMVVKTGDFGISKIL-SSKSKAYTVVGTGTPYLSPEICNKP 179  
 QY 181 YNNKTDINSLGCVLYELCTLKHPPFEGNNLQQLVLCQAHFAPISPGFSRHLHSLSOLF 240  
 Db 180 YNKSQSDIHALGCVLYELASLKEAFEAANLPALVLMKSGTFAPISTRYSPELRQLVLSLL 239  
 QY 241 QVSPDRDRSINSILKRPF-----LENI-----IPKYLTPDEVIGEEFSHMLICRAG 285  
 Db 240 SLEPQRPLPSHMAQPLICIRALLNIHTDVGSRMRRAEKLTP-----G 284  
 QY 286 AFASRHAGVQVKCIQKVRFOGKCPPRSRSVPTK-----RNAILHRNEWR 332  
 Db 285 PPIA--SGSTGRATSACRGVPRGPVPAFPPLPSSVYANGGSLSPRLPMLNTEVVQ 342  
 QY 333 PPAG-AQA---RSIKMI---ERPRTAA 353  
 Db 343 VAAGRTQKAGVTRSGRLILWEAPPLGA 369

Query Match	17.2%	Score 623;	DB 1;	Length 697;	
Best local Similarity	47.0%	Pred. No. 1.8e-26;			
Matches 124;	Conservative	46;	Mismatches 88;	Indels 6;	Gaps 2
QY	1	MDXYDVILKALGOGAFGKAYILAKGSDSKCHVKIKNEFKPIQKEASKKEVILEKMKH	60		
DB	1	MEXYEKTKVGRGAFGVHLCRRTDSALVILKEIPVEQWTRDELAAQNECQVILKLSH	60		
QY	61	PNIVAFPNFQENGRRLPIVMEYCGGDLMKRINRQGVLFSEDOILGWFOISLGLKHIH	120		
DB	61	PNIEIYYENFLDKALMIAMEYAPGGTADYIQKRCNSLLDDETLHSFVQIILALYHVH	120		
QY	121	DRKILHRDKAQNIFLSKNGWAKLGGDFGARVLNNSMELARTCIGTPYLSPEICQNKP	180		
DB	121	NKLLHRDLTKQNLILDKHQYIVKIGDFGISKIL-VSKSKAYTVVGTPCYISPCLCEGP	179		
QY	181	YNNKTDIWSIGCVLYELCTLKHPPGNNLOOLVKICQAHFAPISPGFSRELHSLISOLF	240		
DB	180	YNOKSDIWAIGCVLYELASIKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQILNML	239		
QY	241	QVSPDRPRPSINSILK-----RPFL	259		
DB	240	NLDPSKRPQNEIWAHAICIRPLL	263		
RESULT 10					
NEK2 HUMAN					
ID	NEK2	HUMAN	STANDARD;	PRT;	445 AA.
AC	P51955;				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Serine/threonine-protein kinase Nek2 (EC 2.7.1.37) (Nima-related				
DE	protein kinase 2) (Nima-like protein kinase 1) (HSPK 21).				
GN	NEK2	OR NLK1.			
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
ON	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RC	MEDLINE=22388257; PubMed=12477932;				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,				
RA	Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Zordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Slapchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villaodon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Mveta R.M.,				
RL	Cell Growth Differ. 5:625-635(1994).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RA	Lu K.P., Hunter T.				
RT	"Molecular cloning and expression of NLK1, a human NIMA-like kinase.";				
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RC	MEDLINE=22388257; PubMed=12477932;				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,				
RA	Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Zordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Slapchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villaodon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA					







RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,  
RA Cattolico L., Levy M., Barbe V., De Berardinis V., Ureca-Vidal A.,  
RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,  
RA Sun H., Du H., Pepin K., Antigenave F., Robert C., Cruaud P.,  
RA Bruels T., Jallion O., Friedlander L., Samson G., Brottier P.,  
RA Cure S., Sequens B., Aniere F., Samain S., Crespeau H., Abbasi N.,  
RA Alich N., Boscus D., Dickhoff R., Dora M., Dubois I., Friedman C.,  
RA Gouvenoux M., James R., Madan A., Mairey-Estrada B., Mangerot S.,  
RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B.,  
RA Vacherie B., Belleme C., Belser C., Besnard-Gonnet M.,  
RA Bartol-Mavel D., Boutard M., Bries-Silla S., Combette S.,  
RA Dufosse-Laurent V., Ferron C., Lechaplais C., Louesse C., Muselet D.,  
RA Magdelenat G., Pateau E., Petit E., Sirvain-Trukiewicz P., Trybou A.,  
RA Vega-Czarny N., Battaille E., Bluet E., Bordelais I., Dubois M.,  
RA Dumont C., Guerin T., Haffray S., Hamadi R., Muanga J., Pellouin V.,  
RA Robert D., Wunderle B., Gauguet G., Roy A., Sainte-Marthe L.,  
RA Verdier J., Verdier-Discala C., Hallier L.W., Fulton L., McPherson J.,  
RA Matuda F., Wilson R., Scarcelli C., Gypay G., Wincker P., Saurin W.,  
RA Quetier F., Waterston R., Hood L., Weissbach J.,  
RL "The DNA sequence and analysis of human chromosome 14,";  
[5]  
RN Nature 421:601-607(2003).  
RP SEQUENCE OF 655-979 FROM N.A.  
RC TISSUE:Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusha K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalius D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences,";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Plectotropic regulator of mitotic progression,  
CC participating in the control of spindle dynamics and chromosome  
CC separation. Phosphorylates different histones, myelin basic  
CC protein, beta-casein, and BICD2. Phosphorylates histone H3 on  
CC serine and threonine residues and beta-casein on serine residues.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated  
CC autophosphorylation. Activated during mitosis by intramolecular  
CC by manganese >> magnesium ions. Sensitive to increasing  
CC concentration of detergents. It is not cell-cycle regulated but  
CC activity is higher in G0-arrested cells.  
CC -!- SUBUNIT: Homodimer. Binds to Ran GTPase. Has a greater affinity  
CC for Ran-GDP over Ran-GTP. Interacts with NEX6, NEX7 and BICD2.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: Most abundant in heart, liver, kidney and  
CC testis. Also expressed in smooth muscle cells and fibroblasts.  
CC -!- DEVELOPMENTAL STAGE: Expression varied mildly across the cell  
CC cycle, with highest expression observed in G1 and stationary-phase  
CC cells.  
CC -!- DOMAIN: Dimerizes through its coiled-coil domain.  
CC -!- PTM: Autophosphorylated on serine and threonine residues.  
CC Phosphorylated by CDC2 in vitro.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA  
CC subfamily.  
CC -!- SIMILARITY: Contains 6 RCC1 repeats.  
CC -!- CAUTION: Ref.4 (AAD1936) sequence differs from that shown due to  
CC erroneous gene model prediction.

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CC -----  
DR EMBL; AY048580; AAL05428.1; -;  
DR EMBL; AY080896; AAL87410.1; -;  
DR EMBL; AB082526; BAC02704.1; ALT\_INIT.  
DR EMBL; AC007055; AAD31936.1; ALT\_SEQ.  
DR EMBL; AC007055; AAD31938.1; -;  
DR EMBL; AC007055; AAD31939.1; -;  
DR EMBL; AC007055; AAD31940.1; -;  
DR EMBL; BC009336; AAH09336.1; ALT\_INIT.  
DR Genew; HGNC:18591; NEX9.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR004048; Reg Chr condens.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00415; RCC1; 2.  
DR PRINTS; PR00109; TYRKINASE.  
DR PRODOM; PD000001; Prot kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
DR PROSITE; PS00625; RCC1\_1; FALSE\_NEG.  
DR PROSITE; PS00626; RCC1\_2; FALSE\_NEG.  
DR PROSITE; PS00012; RCC1\_3; 6.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;  
KW Phosphorylation; Cell cycle; Cell division; Repeat; Coiled coil.  
FT DOMAIN 52 308  
FT NP\_BIND 58 66  
FT REPEAT 388 444  
FT REPEAT 445 498  
FT REPEAT 499 550  
FT REPEAT 551 615  
FT REPEAT 616 668  
FT REPEAT 669 726  
FT DOMAIN 732 891  
FT DOMAIN 765 888  
FT DOMAIN 892 939  
FT DOMAIN 752 760  
FT ACT\_SITE 176 176  
FT BINDING 81 81  
FT MOD\_RES 210 210  
FT MUTAGEN 81 81  
FT MUTAGEN 210 210  
FT MUTAGEN 214 214  
FT CONFLICT 351 351  
FT CONFLICT 429 429  
FT CONFLICT 967 967  
SQ SEQUENCE 979 AA; 107149 MW; FF2486CC599322CE CRC64;  
Query Match 14.8%; Score 535.5; DB 1; Length 979;  
Best Local Similarity 40.7%; Pred. No. 1.3e-21;  
Matches 105; Conservative 55; Mismatches 95; Indels 3; Gaps 2;  
QY 4 YDVIKAGQAFGKAYLAKGSKSKHCIVKEINFEKMPICQEKASKVEVLLKMKHPNI 63  
DB 52 YIPTRVLGRGAFGEATLYRTEDDSLWVWKEVDLTRLSKERDALNEIVLALQHDNI 111  
QY 64 VAFENSPQENGRFLIVMEYCDGDLAKRINRQSGVLFSDDIILGWVQLSLGLKHHDHK 123  
DB 112 IAYINFMNDTLLILEVCNGGNLKYDLKLRQDKLFEHEMVVWVLFQVLSAVSCHKAG 171  
QY 124 ILHRDIKAQNIFLSKNGWVAKLGDGFGIARVLNNSMELARTCTIGTPYLSPEICQNKPYNN 183

```

Db 172 ILHRDIKILNPLTKANLI-KLGDYGLAKKLNSEYVAETLVGTPYVSPCLCGVKNF 230
Qy 184 KTDVSLGCVLYELCTLKHPPFEGNNLOQLVLIKICQAHPA--PIPGFSPRELHLSLSQLFQ 241
Db 231 KSDIWAAGCVIFELLTKRTTDTATPLNLCVKIVQIRAMEVDSSQVSLLEIQVHSCLD 290
Qy 242 VSPDRPSPINSILKPPFL 259
Db 291 QDPEQRPTADELLDRPLL 308

RESULT 12
NEK2_MOUSE
ID NEK2_MOUSE STANDARD; PRT; 443 AA.
AC Q35942; O35959;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase Nek2 (EC 2.7.1.37) (Nima-related
DE protein kinase 2).
GN NEK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC STRAIN=Swiss Webster; TISSUE=Testis;
RX MEDLINE=97330684; PubMed=9187143;
RA Rhee K., Wolgemuth D.J.;
RT "The NIMA-related kinase 2, Nek2, is expressed in specific stages of
RT the meiotic cell cycle and associates with meiotic chromosomes.";
RL Development 124:2167-2177(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98243037; PubMed=9583679;
RA Arama E., Yanai A., Kilfin G., Motro B.;
RT "Murine NIMA-related kinases are expressed in patterns suggesting
RT distinct functions in gametogenesis and a role in the nervous
RT system.";
RL Oncogene 16:1813-1823(1998).
RN [3]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=98096235; PubMed=9434622;
RA Tanaka K., Parvinen M., Nigg E.A.;
RT "The in vivo expression pattern of mouse Nek2, a NIMA-related kinase,
RT indicates a role in both mitosis and meiosis.";
RL Exp. Cell Res. 237:264-274(1997)
CC -!- FUNCTION: PROTEIN KINASE THAT IS INVOLVED IN MITOTIC REGULATION.
CC MAY HAVE A ROLE AT THE G2-M TRANSITION. MAY ALSO PLAY A ROLE IN
CC MEIOSIS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with TERF1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN TESTIS. LOW
CC LEVELS FOUND IN MID-GESTATION EMBRYO, OVARY, PLACENTA, INTESTINE,
CC THYMUS AND SKIN. WITHIN THE TESTIS, EXPRESSION RESTRICTED TO GERM
CC CELLS WITH HIGHEST LEVELS DETECTED IN SPERMATOCYTES AT PACHYTENE
CC AND DIPLLOTENE STAGES. ALSO EXPRESSED IN MEIOTIC PACHYTENE OOCYTES.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMA
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U95610; AAB67973.1; -

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DR EMEL; AF013166; AAC35393.1; -
DR ENBL; AF007247; AAB70470.1; -
DR HSPF; P24941; ICRP.
DR MGD; MGI:109359; Nek2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; P800107; PROTEIN KINASE_ATP; FALSE_NEG.
DR PROSITE; P800108; PROTEIN KINASE_ST; 1.
DR PROSITE; P850011; PROTEIN KINASE_DCM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
KW Nuclear protein; Phosphorylation; Cell cycle; Cell division; Meiosis.
FT DOMAIN 8 271 PROTEIN KINASE.
FT NP_BIND 14 22 ATP (BY SIMILARITY).
FT BINDING 37 37 ATP (BY SIMILARITY).
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 175 175 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 443 AA; 51307 MW; DE09565C378307E1 CRC64;

Query Match 14.7%; Score 532.5; DB 1; Length 443;
Best Local Similarity 31.9%; Pred. No. 7.5e-22;
Matches 146; Conservative 92; Mismatches 171; Indels 49; Gaps 15;

Qy 1 MDKYDVKAIGQAFKAYLAKGSDSKHCVIKEIFEKMPIQEKEASKEVILLERMKH 60
Db 5 VEDYEVLSHIGTGYRCQKIRKSDGKILVWKELDYGMTVEKQMLVSEVNLRELKH 64
Qy 61 PHIVAFNSF--QENGRLPVINEYCDGGLMKRN---RQCVLSEQILGNFVQISLG 115
Db 65 PHIVRYDRIIDRTNTTLIVWEYCEGGLASVISKGTDRQYL--EESFVLVRVMTQLTA 123
Qy 116 LKHIDRK-----ILHRDIKAQNIIFLSKNGVMYKLGDFGIARVLNNSMELARTCIGTPY 170
Db 124 LKECHRSDDGHTVLRDLKPNVFLDSKHNV-KLGDGLARILNHDTSFAKTFVGTYY 182
Qy 171 LSPETCONKPYNNKTDVSLGCVLYELCTLKHPPFEGNNLOQLVLIKICQAHPAPISPGFSR 230
Db 183 MSPEQMSCLSYNEKSDIWSLACLLYELCALMPPTAFNQKELAGIRGFRFIPRYSD 242
Qy 231 ELHSLISQLFQVSPDRPSPINSILKRPFLNLIPLYLTPEVIOEBSFHMLI---CRAGAP 287
Db 243 GLNDLITRMFLFKDYHRPSVEILSP-----LIADVAEQRNLBERGRSRSEP 293
Qy 288 AS-RHAGKYVQKCIQKRVFOGKCPP-RSRISVPKRNAILHRNWRPPAGAKARSII-- 343
Db 294 SKLPDSSPVLSELKESQLQDRQALRAREDIQKERELCIRERLAEDKLARAESLMK 353
Qy 344 --ZMTERPILAAVCGHYDYVYACLDM---LERRAHKPSYHIPPOENT---GYEDYQGE 393
Db 354 NVSLKHEHLLCLAGG-----PELDLPSAMKKKVH---FHGESKENTARSENSESYLAK 405
Qy 394 TRHGSPSPQWPAEYLQKFEA---QQYKLVKEVQLGLR 428
Db 406 SKCRLKKELHAAQLRAQALADIENKYQLKSRQILGMR 443

RESULT 13
NEK9_MOUSE
ID NEK9_MOUSE STANDARD; PRT; 984 AA.
AC Q8K1R7; O833P1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase Nek9 (EC 2.7.1.37) (Nima-related
DE protein kinase 9).
GN NEK9 OR NERCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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Db 86 HEENDRLIIVMEFADSGNLDEQI-KLRGSGDARYQOEHEALFLQLCLALDYIHSHKML 144  
QY 126 HRDIKAQNIFLSKNGWAKLGDGFIARVLNNSME--LAETCIGTPYILSPICONKPYNN 183  
Db 145 HRDIKSANVLITSTGLV-KLGDGFGHQYEDTVSGVASTFCGTPYILAPELWNNKRYNK 203  
QY 184 KTDIWSLGCVLVELCTLKHPPGNNLQOLVLKICQAHFAPISPGFSRELHSLISQLFQVS 243  
Db 204 KADVNSLGLVLYEINGMKKPFASNLKGLMSKVLAGTYAPLPDGSFSEFKRWVDGILVAD 263  
QY 244 PDRBSINSILKRPLENLIPKYL-----TPEVIOEEFHHMLICEAGAPASR- 290  
Db 264 PNDRPSVREIFQIPYINKGLFVQALKKNERISDSVKEVLVTQVSEILSEVSFPAHRF 323  
QY 291 -----HAGKVQ----KCKIQKVRF-----QGK 309  
Db 324 LVSQINYDVTHRGVHNKLGNGKSKMKRFLQIVRGQLILTDDEGNPNKGLNLEQVQGA 383  
QY 310 CP-PRS 314  
Db 384 CVPHS 389

Search completed: October 8, 2004, 17:08.08  
Job time : 19 secs





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Db 357 KMSEBAKKRLEFIEKEKKQDQIRFLKAEQMKRQKQRLERINRAREQGRNVLRAGG 416
QY 349 -----PKIAAVCGHYDYVYQALMLRE-BAH-----KPSYHP--IPOE 383
Db 417 SGEVKAFFGIGAVSPSPCSRGQYEHYHAIFDQMLRAEDNEARKWGGIYGRWLPER 476
QY 384 NTG---VEDYGOETRHGSPSPOMPAYEYLQRFPAQYKLYKE-----KQLGLRPS 431
Db 477 QXGHIAVERANQ-----VEEFLQRKEAMONKARAEAGHVYVYLARLQIRLQ--- 522
QY 432 APFNYNQROELR-----SNGEPPRQELPPFKNEMKQBYKQLEERIQOYHN 479
Db 523 ---NFRNQRIKAKURGENKEADGFKQGEAT-EETDMR---LKKMESLKAQTNARAVALK 575
QY 480 DMKEIRKMGKRPENSKISHKTYLVKSNLPPVHODASE-GEAPVQDIEKDKMLQNLQNT 538
Db 576 EQLEKREKAEYEREKVVWEHLVARVKSDDVPLPLELLETGSP----- 619
QY 539 KESKNPEQYKAKGVKFEINLDKCIDSENILQEBEAMDIPNETLT-----FEDGMK 590
Db 620 --SKQVFPVSVTSALKKEVGLDGLTD-----TOBEEMKENSATSKREILRLNENLK 673
QY 591 FREYECVKEHGDTYTKAFELKHCPEAGFSTOTVAAGNRRQWDGAPOTLQOMAVADIT 650
Db 674 AQEDEKEKOH--HSCSETVGHKDEREYETEN-AISSDKKWKMGG-QLVIFPLDAVILDT 729
QY 651 STCPT 655
Db 730 SPSAT 734

RESULT 2
JC7122
Protein kinase (BC 2.7.1.37) 2 - mouse (strain balb/c)
N/Alternate names: serine (threonine) protein kinase
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7122
R:Hayashi, K.; Igarashi, H.; Ogawa, M.; Sakaguchi, N.
Biochem. Biophys. Res. Commun. 264, 449-456, 1999
A:Title: Activity and substrate specificity of the murine STK2 serine/threonine kinase
A:Reference number: JC7122; MUID:20001940; PMID:10529384
A:Accession: JC7122
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-792 <HAY>
A:Cross-references: GB:AJ223071; NID:G4138208; PID:G4138209
C:Genetics:
C:Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Keywords: phosphotransferase

Query Match 18.4%; Score 665.5; DB 2; Length 792;
Best Local Similarity 25.3%; Pred. No. 1.6e-19;
Matches 189; Conservative 137; Mismatches 213; Indels 209; Gaps 23;
QY 4 YDVIRKAGOCAGFKAYLAKGSDSKHCVIKINFEKMPIQEAKSKKEVILLERKHPNI 63
Db 6 YCYMRVVGSGSYGEVTLVKHREDGQYVTKLNLNASSRRERRAAEQEAQLLSQLKHPNI 65
QY 64 VAFNFSQ-ENGRLEFVMEYCDGGLMKRINRQGVLSFSDQILGWFOISLGLKHDR 122
Db 66 VTYKESWEGDGLLYVMGFCGEGDLYRLKLBQKQLPESQVVEFVQIAVALQYLHEK 125
QY 123 KILHRDIKAQNTFLKNGMVAKLPGFIARVLNNSMELARTCIGTPYVLSPEICQNPYN 182
Db 126 HLHRDLKTONVLFRTNII-KVGDGLIARVLNENHGDMASTLIGTPYVMSPELFSNPEYN 184
QY 183 NKTDTWSLGCVLVELCTLKHPPGNNLQVLKIQCAHFAIPISQFSPHLSLSIQFQV 242
Db 185 YKSDVWALGCCVYEMATLKAHFNADKMSLVRIIEGKLPPMPKPVYSTELAEIIRTLSR 244
QY 243 SPRDRPSINSILKRPFLNLI PKYLTPTVQIEQFSHMLIC----- 282

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Db 245 RPEERDSVRSILRQPIKHHISLFLFLEATKAKTSKNVKNCDSRAPKPAVAVVSRKESNTD 304
QY 283 -----RAGAPASRHAGKVKVQCKIOKVRFOG 308
Db 305 VIHYQPRSGEGALHVMGEDKCLSQEKVFDIGPLRSPASLEGHTCK-----QDMNNTG 357
QY 309 K-CPPRSRISVPIKRNAILERNENRPPAGAAQAKARISIKMIE--RPKIAAVCGHYDYVYQAL 365
Db 358 ESCATISIRINIDIL-----PAERRDSANAGVVGESQPCHVDAADEVD---SQC 402
QY 366 DMLRRRAH---KPSYHP---IPOENT-GVEDYGOETRHGSPSPOMPAYEYLQRFPAQ 416
Db 403 STSQEKERLQGNTKSDQGNLLPRSSDGGGEGSELVKPLYPN-----KDKPDDQDQ 457
QY 417 YKLKVKQLGLRP-----SSAEPNPN-----ORQELASNGEERPFQELPPR----- 457
Db 458 VTGIIENQDSIHPRSQPHSSMSSEPSLSRORRQKREQTAHSGTKSQFQELPPLPLPSYPG 517
QY 458 -----KQE-----MKQEYVWKQLEE----- 472
Db 518 IGVKDIATQNDGNGQGGPVAGCVNSRTSTASAKDRPLSARERRRLKQSOEEMLPSPG 577
QY 473 -----IRQVHNDMKIIRKMGKREPEENSKISHK 501
Db 578 AVQRTPSAVEPLKQBEDQPIPAQRPSSDCSITQNNHTLPREKELMHGLSED-ELSSS 636
QY 502 TYLVKSNLPPVHODASEGAPVQDIEKDKMLQMLQ-----NTKES-----KNPEQKYKAK 551
Db 637 T8TDTKSD---GDSREGKSHTNEM-KDLVQLMTQTLREAKESCBDLQVLNPGSEFRLH 691
QY 552 KGVKFEINLDKCIDSENILQEBEAMDIP 579
Db 692 RKYRTDVLVHKGVAEB---VEFHCTELP 716

RESULT 3
I78985
serine/threonine-specific protein kinase (BC 2.7.1.-) STK2 - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Sep-1999
C:Accession: I78985
R:Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmor
Oncogene 9, 1977-1988, 1994
A:Title: Two novel human serine/threonine kinases with homologies to the cell cycle regu
A:Reference number: I58396; MUID:94268838; PMID:8208544
A:Accession: I78985
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-841 <RES>
A:Cross-references: GB:I20321; NID:G348244; PIDN:AAA36658.1; PID:G348245
C:Genetics:
A:Gene: GDB:STK2
A:Cross-references: GDB:374125
A:Map position: 3p21.1-3p21.1
C:Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Keywords: phosphotransferase
F:4-261/Domain: protein kinase homology <KIN>

Query Match 18.3%; Score 660; DB 1; Length 841;
Best Local Similarity 25.3%; Pred. No. 2.8e-19;
Matches 200; Conservative 141; Mismatches 238; Indels 212; Gaps 29;
QY 4 YDVIRKAGOCAGFKAYLAKGSDSKHCVIKINFEKMPIQEAKSKKEVILLERKHPNI 63
Db 6 YCYLRVVGSGSYGEVTLVKHREDGQYVTKLNLNASSRRERRAAEQEAQLLSQLKHPNI 65
QY 64 VAFNFSQ-ENGRLEFVMEYCDGGLMKRINRQGVLSFSDQILGWFOISLGLKHDR 122
Db 66 VTYKESWEGDGLLYVMGFCGEGDLYRLKLBQKQLPESQVVEFVQIAVALQYLHEK 125
QY 123 KILHRDIKAQNTFLKNGMVAKLPGFIARVLNNSMELARTCIGTPYVLSPEICQNPYN 182

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Db 126 HILHDLTKQNVFLRTNII-KVGDGLGIARVLNHCMDASTLIGTPPYMSPELFSNKPYN 184  
QY 183 NKTIDWSLGVLYELCTLKHPPGEGNNLQOLVLKICQAHFAPISQFSLHSLISQLPQV 242  
Db 185 YKSDYVALGCCVYEWATLKHAFNAKMDMSLVYRIEGLPAMPDRDYSPELAELIRTLMSK 244  
QY 243 SPRDPSINSILKRPFLNLPKYLTPVQI-----BEFHHMLICRAGAPAS 289  
Db 245 REEPSPVRSILRQYIKRQISFFLEATKIKTSKNINKNQSGSQKPPFATVV---SGEAB 301  
QY 290 RHAGKVQKQIKQK-----VRPQKC---PPRSRISVPIKRNAILHRNEWPPAGAOKAR 341  
Db 302 NH--EVIHPQLPSLSSGSGTYINGEGKCLSQKPRASGLLKPASL-----KAH 347  
QY 342 SIK--MIERPKAAVCGHYDYVYAOLDMLRRA-----HKPSYHPIPOENTQVE 388  
Db 348 TKQQLSNTELATISS-----VNIDILPAKGRDSVSDGFQENQPRYLNASHELGGIC 401  
QY 389 DYGO-----ETHRGSPS---QW-----PAEYLQKRFQAQYKVK----- 420  
Db 402 SISQVEEMLQDNTKSSAQENLIPWSSDIVTGEKNEPVKPLQPLIKEQKPKDQSLALS 461  
QY 421 -----VEKQLGRP-- 429  
Db 462 PKLECSGITLAHNSRLGSSDPSASRVAGITGVCHHAQDQVAGECIIIEKQRIHPDL 521  
QY 430 ----SSAEPNPN-ORQLRSNGEPR-----FQELPFR-----KN 459  
Db 522 QPHNSGSPSLSRQKREKRETEHRGEKQVRDLFAFQSPPRFLPSHPIVGVKDVTS 581  
QY 460 ENKEQYWKQ-----LEIRQYHNDKX-----IRKNGREPEENSKIHKYIYLVKKS 508  
Db 582 TOKAEENQRRVVTGVSRSRSESSKDRPLSARERRRLKQSQEEMSSGSPS---VRKA 638  
QY 509 NLPVHODASEGAPQD-----TEKDLKQML-----QNTKESKNPEOKY 548  
Db 639 SILV---APGKQPEDQLPARRLSSDCSVTQERKQIHCLSEDLSSSTSTSDKSDGY 695  
QY 549 KAKGVKPEINDKICISDENIL--QEEBAMDIP--NETLTPEDGKMFKEVCEVKEHGDYT 604  
Db 696 GKGQGTNEINALVOLMTQTLDKSCEDVPVAVNPVSEPKLHKRYDTLIL--HGRVA 753  
QY 605 DKAFELHCP 615  
Db 754 EEA-EIHFKE 763

## RESULT 4

T29771  
hypothetical protein ZC581.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T29771  
R:Waterston, B.; Gattung, S.; Le, T.T.  
A:Description: The sequence of C. elegans cosmid ZC581.  
A:Reference number: Z20682  
A:Accession: T29771  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-357 <WAT>  
A:Cross-references: EMBL:AF003134; PIDN:AAB54139.1; GSPDB:GN00019; CBSP:ZC581.1  
A:Experimental source: strain Bristol N2; clone ZC581  
C:Genetics:  
A:Gene: CBSP:ZC581.1  
A:Map position: 1  
A:Introns: 31/3; 81/1; 120/3; 186/1; 226/3; 260/1; 288/3  
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology  
Query Match 15.7%; Score 569; DB 2; Length 357;  
Best Local Similarity 40.9%; Pred. No. 4.9e-16;  
Matches 113; Conservative 59; Mismatches 90; Indels 14; Gaps 4;

QY 1 MDKYDVIKAIQAGAFKAVLAKGKSDSKH--CVIKENFEKMPIQEKASKKEVILLEKM 58  
Db 1 MDYKRVVVGAFGVGVCWLCRGKNDASHQKVIILINHTGTEKEENSIQSEVNLKKV 60  
QY 59 KHNIVAFNPSFQENGRFLFVMEYCDGGDLMKRINQGV-----LFSDDILGWFWQ 111  
Db 61 QHPLITGYIDSFIDNQLGIVMCYASGGTLERLINDQRAIKDSNNREYFPEKTVLDYFTQ 120  
QY 112 ISLGLKHIDHRDLHRDIKAQNIFLSKNGWVAKLGDGFIARVLNNSMELARTCIGTPPYL 171  
Db 121 ILTALNHQKNIHVHDLKPNILMNRKTVLKLSDFGISKEL-GTKSAASVTIGTPNYL 179  
QY 172 SPEICQNKPNYNTDWSLGCVLVELCTLKHPPGEGNNLQOLVLKICQAHFAPISQFSSRE 231  
Db 180 SPEICSRPNYQKSDWMSLGCVLVELCTLKHPPGEGNNLQOLVLKICQAHFAPISQFSSRE 239  
QY 232 LHSLSISQLFQVSPRDRPSINSILKRPFLNLPKYL 267  
Db 240 VKMLVENLLKTHTKRPDVSQLSDP-----LVLPYL 271

RESULT 5  
G01452  
NIMA-like protein kinase 1 - human  
C:Species: Homo sapiens (man)  
C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C:Accession: G01452  
R:Lu, K.P.  
A:Reference number: G07172  
A:Accession: G01452  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-445 <LUX>  
A:Cross-references: EMBL:U11050; NID:G507874; PIDN:AAA19558.1; PID:G507875  
C:Genetics:  
A:Gene: NLK1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C:Keywords: ATP  
F:6-271/Domain: protein kinase homology <KIN>  
F:14-22/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 539.5; DB 2; Length 445;  
Best Local Similarity 29.9%; Pred. No. 8.6e-15;  
Matches 141; Conservative 88; Mismatches 167; Indels 75; Gaps 13;

QY 2 DKYDVIKAIQAGAFKAVLAKGKSDSKHCVIKENFEKMPIQEKASKKEVILLEKMHP 61

Db 6 EDYEVLYTIGTSGYGRQKIRKSDGKILYWKELDYGSMTAEKQMLVSEVNLRELKHP 65

QY 62 NIVAFNSF--QENGRFLFVMEYCDGGDLMKRI---NRQGVLFSEDDILGWFWQISGL 116

Db 66 NIVRYDRIIDRTNTLLIYVMEYCEGGDLASVITKGTKEQYL-DEEFVLVMTQLTLAL 124

QY 117 KHIHDRK-----ILHRDIKAQNIFLSKNGWVAKLGDGFIARVLNNSMELARTCIGTPPYL 171

Db 125 KECHRRSDGGHTVLHRDLKDPANVFLDGQNV-KLGDPLGLARILNHDTSFAKTFTGTPPYM 183

QY 172 SPEICQNKPNYNTDWSLGCVLVELCTLKHPPGEGNNLQOLVLKICQAHFAPISQFSSRE 231

Db 184 SPEQNRMSYNEKSDIWSLGLLYELCALMPPTATFSQKELAGIKREGKFRRIPIRYVSD 243

QY 232 LHSLSISQLFQVSPRDRPSINSILKRPFLNLPKYL 267

Db 244 LNEIITRLNLKDYHRPSVEILENPLIADL-----VADEQRNLNRRGRQLGEPE 294

QY 288 ASRHAGKVQKQIKQKVRFGQKPPRRSRIVPDKRNAILHRNEWPPAGAOK----- 339

Db 295 KSDSSPVLSELKKEIQLO-----EREALXAREERLEQKEQLCVRERLA 341

QY 340 -----ARSTKMTREPKIAAVCGHYDYVYAQLDMLRRRAHPSYHPIPOENTGVSD 389

Db 342 EDKLAREANLLKNYSILKERKFLSLANPELLNLPSSVIKKVH---FSGESKENI----- 394



A;Cross-references: EMBL:Z98975; PIDN:CA01153.1; GSPDB:GN00066; SPDB:SPAC19E9.02  
A;Experimental source: strain 972h-; cosmid c19E9  
C;Genetics:  
A;Gene: SPDB:SPAC19E9.02  
A;Map position: 1  
A;Introns: 20/3; 28/3  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C;Keywords: phosphotransferase; protein kinase

Query Match 14.1%; Score 511; DB 2; Length 722;  
Best Local Similarity 24.8%; Pred. No. 1.7e-13;  
Matches 182; Conservative 126; Mismatches 273; Indels 152; Gaps 27;

QY 1 MDKYDVLKATCGAGAGKAYLAKGSDSKHCVIEKINPEKMPIOEKASKEVILLKMKH 60  
DB 1 MEKILIECCHGSGFGRYKQRLKOGALLAQKEIHFGNITROEKQVIADENVILRNKXH 60  
QY 61 PNIVAFNPSQENGR-----LFIYMEYCDGGDLMKRINR--QRGVLFSEDOILGWFIQISL 114  
DB 61 PNIVQYCG--BELNRSQVNLNMYEYCGHGLANLIQRYKEEKRFTEQVLAFFQLLL 118  
QY 115 GLXHH-----DKILHRIKAIQNIFLSXNGMAKLGDFGIARVLN 155  
DB 119 ALYRCHYGENAPACDSQWPBEI FHPKQSVLHRIKIPANI ELDENNSV-KLGDGLSKLLD 177  
QY 156 NSMELARTCTGTPYLSPEIKONKPYNNKTDIWSLGCVLVELCTLKHPPPEGNNLQQLVLK 215  
DB 178 NTRVFTQSYVGTPTYMSPEILIRSPYSAKSDVWALGCVIEI CMLTFPEGRSYLSLQRN 237  
QY 216 ICQAHFAPISPGFSERLHLSISQLFQVSPDRDRPSINSILKRPFLENLIPKYLTPVIOBE 275  
DB 238 ICQGNLSCWDHHYSDDVFLIRHCLVNSDLRPTTYQLLRSPILSDIRSKLESERVVLEQ 297  
QY 276 FS-----HMLICRAGAPASHAGKVQVKCKI QKVRPQCKPPRSRISVPIKENAILHRN 329  
DB 298 SLLHKXHQMLQLENDLQFREQLSARELENV-----IASRLA---QREILRRE 347  
QY 330 EMRPPAGAQAARSIKMERPKIAAVCGHYDYIYAQL--DMLRRRAHKPSYHPQPENTGV 387  
DB 348 -----LEK-QLRDMDARYQRHMQTVNMQKRVTSFVDHNEQPESSTA 390  
QY 388 EDYQETRHGPSQSWPAEVLQRFKAQVYKLVKEQL-----GLPSSAEFNYNQ--- 438  
DB 391 EMFVDCITIEA--SQSPLLHP-----KLGISKPLQTLSCPGFTLTTCQBPILKRPTL 439  
QY 439 RQELNRNGEPRFQELFPRKN--EMKQEYWK--QLEIRQQ--YHNDMKKIRKMGREP 492  
DB 440 RKLSSRALHTTATLMKYRANASSLRTPIDKQGITSLQCKNGTSNQVADCNKLLHTS 499  
QY 493 EENSKI SHKTYL-----VKKSNLPVHOD-----ASEGEAPVQD----- 525  
DB 500 LDGKKLSPELNCNKFSGDEGLPNRKVKSLSVESDETAVSASSGESVPTDSTLDTTKSKSV 559  
QY 526 -----IEKDLQKMLQNTKESKNPEQYKAKKV-----KPEINLDKICSD 567  
DB 560 FVHPSPQSILYVEK-LEKLIARSDVSK-PSKASKTLHGVALPSLPYDVHAEKIARE 617  
QY 568 NILQ-----BEERAVDIPNETLTFEDGMKFKEYECVKEHGSDYTDKAFELHCP 615  
DB 618 NEMDGNFKTMKINQHPDEYVLRTPKKIQLLE-GOKRSP---VKQLGRGLGNKLLRRSAMD 673  
QY 616 AGFSTQTVAAVGN 628  
DB 674 AGLELRKAATSN 686

RESULT 9  
JC7838  
Nek6 protein kinase, NIMA histone H3 kinase homolog - human  
C;Species: Homo sapiens (man)  
C;Date: 09-Dec-2002 #sequence\_revision 09-Dec-2002 #text\_change 31-Mar-2003  
C;Accession: JC7838  
C;Hashimoto, Y.; Akita, H.; Hibino, M.; Kohri, K.; Nakanishi, M.

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QY 151 ABVLNNSMELARTCTGTPYLSPEIQNPKYNTDINSLGCVLYELCTLKHPEGNLQ 210
Db 183 SKVM-OSHDFASTYVGTTFYMSPEICAAEKYTLKSDIWSLGCIIYELCARPPFNATHY 241
QY 211 QLVKICQAHFAPISPGFSRELHSISQFVSPDRPSINSIIKRPPLNLIKYLTPE 270
Db 242 QLVQKIKEGIAPLPSVYSGELFATIKDCLRVNDRPDATLLNLP-----IVRLMKE 296
QY 271 VIQEFSEHMLICRAGAPASRHAGVKVQCKKQKVFQKQCPKRSISVIPKRNAILHNE 330
Db 297 KEWFEFRTL-----RTKEETLNK-RIRELDSKLASLETESKSSRAEIDASL-RRE 345
QY 331 WRPPAGAOKARSIMIERPKTAAVCHGYDYVYQAQDMLRRRAHKPSYHPIQENTGVEDY 390
Db 346 WE-----VKAR-----LEIDL-----VAQE----- 361
QY 391 GOETHRSPSPOMPAEYLQKPEAQYKLVKQKQ-----GLRP-----SSA 432
Db 362 -----IESLQKQKE-GEVQARVEAELOHGRGPMFNSHGQGSFSTAATL 406
QY 433 BBNVQORQLRNGEPRFQELPFKKNEMKEQYWKQLEERQQVHNDMKIRKMGREP 492
Db 407 VSDYNLSSVSGSGGDFPSTTD-----ITDISIAESTDGSITTKIPPT 450
QY 493 EENSISHTKY--LVKKNLPHVDAS--EGEAPVQDIEKDLQKMLQNTK-ESKNPEQKY 548
Db 451 FHRA---QTSYSSAPAESVLGTGPMDIEMASPTIASLSLSPRMALTKAPTTPRMIF 506
QY 549 KAKGVKFEINLDKICSDENILQEEBAMDIPNETLTPEDG 588
Db 507 -----GEEPTSTDKSNWEVRETEMIDSG 530

RESULT 11
T49136
protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: protein F26G5.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49136
R:P/Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25017
A:Accession: T49136
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-941 <BAN>
A:Cross-references: EMBL:AL353814; GSPDB:GN000061; ATSP:F26G5.150
A:Experimental source: cultivar Columbia; BAC clone F26G5
C:Genetics:
A:Gene: ArSP:F26G5.150
A:Map position: 3
A:Introns: 33/2; 55/3; 77/3; 93/2; 108/3; 135/3; 150/1; 166/3; 194/1; 210/3; 218/3; 237/3
Query Match 12.7%; Score 457.5; DB 2; Length 941;
Best Local Similarity 23.4%; Pred. No. 2.7e-11;
Matches 152; Conservative 121; Mismatches 235; Indels 141; Gaps 21;
QY 1 MDKYDVIRKAIGAGAGKAYLAGKSDSKHCIVKEINFEKMPIOKEASKKEVILLKMK 60
Db 5 MDQYELMEQIGRAGFAAILVHHAERKKYVLKTLARQTERCRRSAHQMSLIARVQH 64
QY 61 PNIVAFNSFQNG-RLFTVMEYCDGDLMKRINRQKGLVPSQDQLMGVQISLGLKHI 119
Db 65 PIVFEKAWKGVYCVITVCGGGDAELMKSNVYFPEKLCWFTQLLAVEYL 124
QY 120 HPRKILHRDIKAQNIFLSKNGMAVLGDFGIARVANNMEIARTICIGTPYLSPEIQN 179
Db 125 HSNYVLRDLKCSNIFLTAKQDV-RLGDFGLAKTL-KADDLTSSVVGTPNTMCPPELLADI 182
QY 180 PYNNTDINSLGCVLYELCTLKHPEGNLQOLVLKIQAHFAPISPGFSRELHSLISQL 239
Db 183 PYGFKSDIWSLGCIIYEMAAYRPAKAFDMAGLISK-----KSTH----- 222
QY 240 FVSPDRPSINS-----ILKRPFLNLI PKY-----LTPE----- 270
Db 223 -QCNVKEEPRVSAKRWASBILKHPYLOPYVEQYRPTLSAASITPEKPLNSRGRSMAES 281
QY 271 -----VIQEFSEHMLICRAGAPASR-----HAGVVQCKKIQKVR 305
Db 282 QNSNSSEKDNFVSDKNIRYVVPNGKVTETDSDGFDVDEDLHVQCSAENGNLQSV- 340
QY 306 FQKCPKRSISVIPKRNAILHNEWRP-----PAGAOKARSTMIERPKIAAVCHGYDY 361
Db 341 -SATKPDGHIKLPV-----HSQRPDVIQPRHPKTIKRNIMVLMKEEKAENG----- 387
QY 362 YAQDMLRRRAHKPSYHPIQENTGVEDYQETHRSPSPOMP-----AEYLQKFEAQ 416
Db 388 -----SPMRNRRSPS--SVPTQKNV-----TPSKIPKLGDIASHSKTNASTPI 431
QY 417 YKLKVEKQGLRPSSEPNYQORQLRNGEPRFQEL-----PFRKNEMKEQYWKQLEBI 473
Db 432 PPSKLASDSARTPGSPFKHPMPVIDSSPKLRPNDRISPSPAKKEAEFA----- 482
QY 474 RQYHNDMKEIRKMGREPEENSKISHKTYLVKK--SNLPVHQDASEGAPVQDIEKDLK 531
Db 483 -----MSVRRGRQTPPTLPARTSLIAHQRLQCADISNMAKETAKLHPSVSESETSNH 537
QY 532 QMELQNTKSKQPEQK---YKAKGVKFEINLDKICSDENILQEEBAMD 577
Db 538 QSRVHASPVSTTPEPKRTSVGSAKGMQSESS--NGISSLSLQAFELCD 584

RESULT 12
T21075
hypothetical protein F19H6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T21075; T21124
R:McMurray, A.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19368
A:Accession: T21075
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-294 <WIL>
A:Cross-references: EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN000028; CESP:F19H6.1
A:Experimental source: clone F17E5
R:McMurray, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19378
A:Accession: T21124
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-294 <W12>
A:Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN000028; CESP:F19H6.1
A:Experimental source: clone F19H6
C:Genetics:
A:Gene: CESP:F19H6.1
A:Map position: X
A:Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C:Superfamily: kinase-related transforming protein; protein kinase homology
Query Match 11.7%; Score 424; DB 2; Length 294;
Best Local Similarity 37.1%; Pred. No. 2e-10;
Matches 85; Conservative 55; Mismatches 93; Indels 6; Gaps 4;
QY 1 MDKYDVIRKAIGAGAGKAYLAGKSDSKHCIVKEIN-PEKMPIOKEASKKEVILLKMK 59
Db 20 LEUFIETKIGKQGVSEVFRQCTWDLHLVALUK:QVEMVDQKARQDCLKIDLLKQLN 79
QY 60 HPNIVAFNSFQNGRLFTVMEYCDGDLMKRIN--RQRGVLFSDQILMGVQISLGLK 117
Db 80 HYNVIRYASFIDNNQNLNIVLELAGDMSRMKHPKKGRLIPEKTIWKVQVLARALA 139

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Qy	3	KYDVIKAIGOGAFGKAYLAGKSDSKCHVTKENFEMKPIQEKASAKKEVILLKMKHPN	62
Db	24	EYQVLBEIGRSGSPVRKVTHIPTKLLVRKD;KYGHMNSKERQQLIAECISILSQLKHEN	83
Qy	63	IVAFFN-SFOENGR-LFIVMEYCDGGDLMKRIN--RQGVLFSEDDOILGFVQISLGLKH	118
Db	84	IVZFYKWDPEQKEVLYLYNEYCSRGDLSOMIKHYQEHKYYIPEKIVGWGLAQLLTALYK	143
Qy	119	IH-----DRK-----ILHRDIKAQNIPLS-----	137
Db	144	CHYGVSELPULTTIYDRMKPPVKGNIVIRHDLKPGNIFLSYDDSDYNINQVDPGHEEVNS	203
Qy	138	-----KNG-----MWAKLGDGFIARVLNNSMELARTCTIGTPYVLSPEICQNK	179
Db	204	NYVEDHRVNSGKKGSPMDYSQVVVKLGDGFLAKSLSTISQFATYVYGTPTPYSPEVLMQ	263
Qy	180	PNYKNTDIIWSLGCVLVELCTLKHPPFGNNLQQLVLIKIQAHFAPISPGFSREHLHLSIQ	239
Db	264	FYGLSDIIWSLGCVIPEMCSLHPFPAQKYLELQTKIKNGKCDTPVEYVYSGNLAIHSM	323
Qy	240	FQVSPDRPSINSILKRPFLNLI PKVLPTEVIOEBFESHMLICRAGAPASRHAGKV---	296
Db	324	IDVNLATRS-----TFELLQD--IQIARTAKSLQLEFRPEKLLDYE	363
Qy	297	-QKCKTKQVRFOGKCPFRSRISVPIKRNAILHNRW-----PPAGAQAARSIKMIERP	349
Db	364	NELTNIEKI-----LEKQAIERYELSQLKEQFTQAVEERAREV--ISGK	406
Qy	350	KIAAVCGHYDYVYAAQLDMLRRRAHKPSYH	378
Db	407	KVKGVPEISINGYV-----KKPAKPAYH	429
RESULT 14			
B96587			
hypothetical protein F20D21.33 [imported] - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001			
C:Accession: B96587			
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;			
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D			
ansen, N.F.; Hughes, B.; Huizlar, L.			
Nature 408, 816-820, 2000			
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.			
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; M			
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.			
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;			
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.			
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.			
A:Reference number: A86141; MUID:21016719; PMID:11130712			
A:Accession: B96587			
A:status: preliminary			
A:molecule type: DNA			
A:Residues: 1-200 <STO>			
A:Cross-references: GB:AE005173; NID:94585993; PIDN:AAD25629.1; GSPDB:GN00141			
C:Genetics:			
A:Gene: F20D21.33			
A:Map position: 1			
Query Match 11.5%; Score 415.5; DB 2; Length 200;			
Best Local Similarity 40.5%; Pred. NO. 3.1e-10;			
Matches 79; Conservative 51; Mismatches 62; Indels 3; Gaps 3;			
Qy	1	MDKYDVYIKAGOGAFKAYLAGKSDSKCHVTKENFEMKPIQEKASKEVILLKMKH	60
Db	1	MEQYEFLEQIGKSGFSGSALLVRHKEKKVYKIRLARQTRRSAAHQEVGLSKVRH	60
Qy	61	PNIVAFNSFOENG-RLFIVMEYCDGGDLMKRINRQGVLFSEDDOILGFVQISLGLKHI	119
Db	61	PFTVEYKDSWKEACVVCVIVGICEGDDWAQATKSGNVHFOBEKLCRWLQVLLMLEYL	120
Qy	120	HDKRLIHRDIKAQNIPLSNGMVAKLGDGFIARVLNNSMELARTCTIGTPYVLSPEICQNK	179

121 HSNHILHRDVKCSNIFLTKEODI-RLGDFGLAKIL-TSDDLTSSVVGTPSYMCPELLADI 178

Qy 180 PYNKTDIWSLGCVL 194

Q7	I I A N I D W S L G T F E L 193
D8	P Y G S K S D I W S L G T F E L 193

RESULT 15

T47988

serine/threonine-protein kinase-like protein - Arabidopsis thaliana

N;Alternate names: protein F21E14.130

C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
N/A:Accession names: Protein F21F14.130

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 20-Apr-2000

C; Date: 20-Apr-2000  
C; Accession: T47988

C/Accession: T4/988  
R/Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiquenave, F.; Sa

R; Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cat  
submitted to the Protein Sequence Database. February 2000

A:Reference number: Z24481

A;Reference number:  
A:Accession: T47988

A;Accession: T47988  
A;Status: preliminary

A;Status: preliminary  
A:Molecule type: DNA

A;Molecule type: DNA  
A:Residues: 1-648 <CHO>

A;Residues: 1-648 <CHO>  
A:Cross-references: EMBL:AI138642

A; Cross-references: EMBL:AL138642  
A: Experimental source: cultivar Columbia; BAC clone F21E14

A; Experiment  
C; Genetics:

C;Genetics: 3  
A;Men position: 3

A;Map position: 3

A; Introns: 77/3; 11

Query Match 11.3%; Score 410; DB 2; Length 648;

Query Match 11.3%; Score 410; ES 2;  
Best Local Similarity 34.2%; Pred. No. 1.4e-09;

Best Local Similarity 34.2%, Freq. NO: 1.4E-05;  
Matches 94; Conservative 56; Mismatches 111; Indels 14; Gaps 7;

10 IGOGAFGKAYLAKGKSDSKHCVTKEINFEEKMPIOEKEASKKEVILLLEKMKHPNIVAFFNS 69

QY IGQAGFGRAY LARGKSDSKHCV LKEINFENMPTQKEASKREV LLENKWKHFNIVAFNS 69

Db 16 ICGSFAVWLAKHRSSGLEVAVKIDKLLSPKVRDNLKEISILSTIDHPNIIRFYE 75

70 BAENCBI ETUMBYCNCOCBI MYB INPBOCIV ESEBOI CBEV-OTSI CI KYTHDPKTI LHPD 128

[illegible]

Db 76 IETGDRIFLVLEYCSGGDLAGYINRHGKV--PEAVAKHFMRLALGLQLVLEKHFIFHRD 132

QY 129 IKAQNIFLSKNGM--VAKLGDFGIARVLNNSMELARTCIGTPYYLSPEICQNKPYNNKTD 186

[illegible]

DD UNFQNULESSNEVIFLEUNIGUFGFARSLIFE-SMAETFCGSGFUMTAFETINQXNDI DAAAD 131  
133

187 IWSLGCVLVELCTLKHPFEGNNLOOLVLKICOAHFAPISPGFSRELH---SLISOLFOV 242

Search completed: October 8, 2004. 17:09:32

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Job time : 25 secs